

PATENT COOPERATION TREAT

PCT

REC'D 0 9 NOV 1999

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INTERNATIONAL PRELIMINARY EXAMINATION REPORT

(PCT Article 36 and Rule 70)

Applicant's or agent's file reference	Se Se	e Notificatio	on of Transmittal of International	
PHM 70251/WO FOR FURTHER ACTION Preliminary Examination Report (Form PCT/IPEA/416)				
International application No. International filing date (day/month/year) Priority date (day/month/year)			Priority date (day/month/year)	
PCT/GB98/02259	28/07/1998	c	01/08/1997	
International Patent Classification (IPC) or na C12N15/00	ational classification and IPC			
Applicant				
ZENECA LIMITED et al.				
This international preliminary exam and is transmitted to the applicant a	ination report has been prepared by according to Article 36.	this Intern	ational Preliminary Examining Authority	
2. This REPORT consists of a total of	8 sheets, including this cover sheet			
 □ This report is also accompanied by ANNEXES, i.e. sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT). These annexes consist of a total of sheets. 				
3. This report contains indications relating to the following items: □ ☑ Basis of the report □ ☑ Priority				
III Son-establishment of opinion with regard to novelty, inventive step and industrial applicability				
IV □ Lack of unity of inventi				
V 🖾 Reasoned statement u	The state of the s			
VI 🕏 Certain documents cit	ted			
VII 🔲 Certain defects in the i	international application			
VIII 🖾 Certain observations o	on the international application			
Date of submission of the demand		pletion of th		

Date of submission of the demand

08/02/1999

Name and mailing address of the international preliminary examining authority

Date of completion of this report

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M

European Patent Office D-80298 Munich

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International application No. PCT/GB98/02259

1. This report has been drawn on the basis of (substitute sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to the report since they do not contain amendments.): Description, pages: as originally filed 1-13 Claims, No.: as originally filed 1-21 Drawings, sheets: 1/19-19/19 as originally filed 2. The amendments have resulted in the cancellation of: ☐ the description. pages: ☐ the claims. Nos.: ☐ the drawings, sheets: 3.

This report has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed (Rule 70.2(c)): 4. Additional observations, if necessary: II. Priority 1.

This report has been established as if no priority had been claimed due to the failure to furnish within the prescribed time limit the requested: copy of the earlier application whose priority has been claimed. ☐ translation of the earlier application whose priority has been claimed. 2.
This report has been established as if no priority had been claimed due to the fact that the priority claim has

been found invalid.



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Thus for the purposes of this report, the international filing date indicated above is considered to be the relevant date.

3.	Add	itional observations, if necessary:
	see	separate sheet
III.	Nor	-establishment of opinion with regard to novelty, inventive step and industrial applicability
Th or	e qu to be	estions whether the claimed invention appears to be novel, to involve an inventive step (to be non-obvious). e industrially applicable have not been examined in respect of:
		the entire international application.
	\boxtimes	claims Nos. 14,15, 16.
be	caus	e:
		the said international application, or the said claims Nos. relate to the following subject matter which does not require an international preliminary examination (<i>specify</i>):
		the description, claims or drawings (indicate particular elements below) or said claims Nos. are so unclear that no meaningful opinion could be formed (specify):
	⊠	the claims, or said claims Nos. 14 are so inadequately supported by the description that no meaningful opinion could be formed.
	\boxtimes	no international search report has been established for the said claims Nos. 15, 16.



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V. Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

1. Statement

Novelty (N)

Yes

Claims 3, 12, 13, 17-20

No:

Claims 1, 2, 4-11, 21

Inventive step (IS)

Yes.

Claims none

No:

Claims 1-13, 17-21

Industrial applicability (IA)

Yes:

Claims 1-13, 17, 18, 20, 21

No: Claim

Claims 19 (reserved opinion)

2. Citations and explanations

see separate sheet

VI. Certain documents cited

1. Certain published documents (Rule 70.10)

and / or

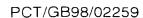
2. Non-written disclosures (Rule 70.9)

see separate sheet

VIII. Certain observations on the international application

The following observations on the clarity of the claims, description, and drawings or on the question whether the claims are fully supported by the description, are made:

see separate sheet



EXAMINATION REPORT - SEPARATE SHEET

II. PRIORITY

This first preliminary written opinion has been established considering the priority 1) date 01.08.97 as a valid date. The Applicant is reminded that documents: WO 97 37223 A (UNIV NORTH CAROLINA) 9 October 1997 OHARA O. ET AL. in EMBL DATABASE, 5 December 1997 cited in the international search report may become relevant after consideration of the priority document which is unavailable at present.

III. NON-ESTABLISHMENT OF OPINION

- The subject-matter of Claim 14 is not supported by the description and thus, it is 2) not amenable to examination of novelty, inventive step or industrial applicability. Said claim relates to a method for identifying a compound capable of modulating the activity of a ZGGBP1 protein. However, a function of said protein has not been demonstrated. Sequence analysis of the encoding gene has revealed several structural domains which correspond to several potential functions (p. 2). Furthermore, sequence homology of the encoding gene with at least two different genes, nedd-4 and Pub3, indicates even more potential functions (p.3). The application as filed, does not provide any indication as to which of all the potential activities of ZGGBP1 the method of Claim 14 is directed to. Since the method of said claim is not supported by the description, an opinion cannot be established.
- No opinion is established for the subject-matter of Claims 15 and 16 because 3) said claims relate to inventions in respect of which no international search report has been established (Rule 66.1(e) PCT).

V. REASONED STATEMENT UNDER ARTICLE 35(2)

The present application relates to the isolation of a cDNA clone comprising the 4) sequence presented in SEQ ID NO1, called gene ZGGBP1. Said sequence resides, along with many other expressed sequences, in the 18q21 chromosomal region which was shown previously to be associated with the neurological disorder bipolar affective disorder. The ZGGBP1 gene sequence appears to have 85% identity at the amino acid level with the human gene encoding nedd-4 which



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was shown previously to be a negative regulator of a sodium channel which is deleted in Liddle's syndrome (a hereditary form of hypertension). The ZGGBP1 gene sequence shares also 100% identity, over a 3kb region, with the previously identified gene, Pub3 which may be involved in regulation of cell cycle of eukaryotic cells. The Applicant has not demonstrated that said ZGGBP1 gene has any function.

5) The subject-matter of **Claims 1, 2, 4-11, 21** is not novel as required by Article 33(2) PCT.

Claim 1 relates to a polynucleotide comprising a nucleic acid sequence encoding the polypeptide of SEQ ID NO 2, and homologues and fragments.

Figure 2 of the present application discloses the amino acid sequence of the known human nedd-4 gene which is 85% homologous to polypeptide of SEQ ID NO 2 (p.11). Figure 5 of the present application discloses the nucleotide sequence of the known gene Pub-3 which comprises fragments up to 3 kb long which are identical to the polynucleotide encoding SEQ ID NO 2.

Thus, the subject-matter of said claim has been disclosed in the prior art.

Similar arguments apply for the subject-matter of Claims 2, 4-11, 21.

6) The subject-matter of **Claims 3**, **12**, **13**, **17-20** is not inventive as required by Article 33(3) PCT.

Said claims refer to subject-matter as defined in Claims 1-7, 10 or 11 and comprise additional technical features which may render said subject-matter novel. However, said technical features represent standard options available to the skilled person aware of the state of the art in the field of gene technology. Thus, said technical features do not impart any inventiveness to said subject-matter. Consequently, even if it is assumed that the subject-matter of Claims 3, 12, 13, 17-20 is novel, said claims do not comprise an inventive step.

7) Claim 19 is directed to the use of a polynucleotide in gene therapy. Said claim is



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thus, considered to be directed to method of treatment of the human or animal body. For the assessment of claims as far as they are directed to a method of treatment of the human or animal body or to a diagnostic method practised on the human or animal body, no unified criteria exist in the PCT, on the question whether they are industrially applicable. The patentability can be dependent upon the formulation of the claims.

VI. CERTAIN DOCUMENTS CITED

8) The following documents are cited under Rule 70.10 PCT WO 97 37223 A, 9.10.97, filed 03.04.97, with priority date of 03.04.96

VIII. CERTAIN OBSERVATIONS ON THE INTERNATIONAL APPLICATION

- 9) The Applicant is reminded that the claims must be comprehensible from the technical point of view and clearly define the object of the invention, that is to say indicate all the essential features thereof (Rule 6 PCT). The subject-matter of Claims 3, 7, 17 and 21 does not fulfil this condition, as the claimed nucleic acid is only defined by the name of the encoded protein "ZGGBP1" without disclosing any technical feature which unambiguously characterizes the claimed subject-matter. A gene being a chemical product should be clearly defined by its formula i.e. its nucleotide sequence.
- 10) Claim 1 is drafted towards an isolated nucleic acid with specified sequence content. However, the function of said nucleic acid is not clearly stated in the claim.

The Applicant speculates in the description that said nucleic acid encodes a protein which may be associated with the bipolar affective disorder although no evidence for such association is presented. Furthermore, even if such an association of the claimed protein with the bipolar affective disorder is established, a function of the protein is not defined nor could be speculated, especially since sequence analysis of the protein appears to indicate several potential functions. Since there is no conclusive demonstration of any function of the polypeptide of SEQ ID NO 2, as such, any function can, at best, be accepted as speculative. At



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this point, it is not apparent what problem said polypeptide or fragments thereof are intended to solve or whether said sequences represent a solution comprising an inventive step. Insufficient disclosure of essential technical features, such as the function of a given nucleotide or amino acid sequence, does not allow for the acknowledgement of an inventive step involved in solving a technical problem. The lack of sufficient disclosure of the invention is contrary to Article 5 PCT and makes it difficult if not impossible to examine the novelty and inventive step of the claimed invention.

The same arguments apply to the subject-matter of Claims 2-7 and 10-12.

11) The subject-matter of Claim 11 is not clear as required by Rule 6 PCT. Said claim relates to a polypeptide comprising the amino acid sequence of SEQ ID NO 4. As said sequence is being disclosed only in the sequence listing without any mention of it in the description, it is not entirely clear what relation it bears with the invention as disclosed in the present application.



INTERNATIONAL SEARCH REPORT

Internat. Application No PCT/GB 98/02259

CLASSIFICATION OF SUBJECT MATTER PC 6 C12N15/00 C07K A. CLASS C07K14/435 C12N9/10C12Q1/68 According to International Patent Classification (IPC) or to both national classification and IPC **B. FIELDS SEARCHED** Minimum documentation searched (classification system followed by classification symbols) IPC 6 C07K C12N Occumentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practical, search terms used) C. DOCUMENTS CONSIDERED TO BE RELEVANT Category Citation of document, with indication, where appropriate, of the relevant passages Relevant to claim No. X.P WO 97 37223 A (UNIV NORTH CAROLINA) 6.10. 9 October 1997 12 - 14. 18-21 Α see abstract 1,2,4 see page 9, line 1 - page 10, line 23 see figure 23 see claim 48 see Nos.125 and 126 of Sequence Listing X,P OHARA O. ET AL.: "Prediction of the 1,2,4. sequences of unidentified human genes. 8-10,18, VIII. The complete senguences of 77 new cDNA clones from brain which can code for large proteins in vitro" EMBL DATABASE.5 December 1997, XP002087609 HEIDELBERG. DE AC: AB007899 -/--X Further documents are listed in the continuation of box C X Patent family members are listed in annex Special categories of cited documents "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory, underlying the "A" document defining the general state of the lart which is not considered to be of particular relevance. invention "E" earlier document but published on or after the international "X" document of particular relevance; the claimed invention filing date cannot be considered novel or cannot be considered to "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another involve an inventive step when the document is taken alone "Y" document of particular relevance, the claimed invention citation or other special reason (as specified) cannot be considered to involve an inventive step when the document is combined with one or more other, such documents, such combination being obvious to a person skilled "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but in the art later than the priority date claimed '&" document member of the same patent family Date of the actual completion of the international search Date of mailing of the international search report 11 December 1998 12/01/1999 Name and mailing address of the ISA Authorized officer European Patent Office, P.B. 5818 Patentiaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040. Tx 31 651 epo ni. Fax: (+31-70) 340-3016 Panzica. G



INTERNATIONAL SEARCH REPORT



Internal Application No PCT/GB 98/02259

		PCT/GB 98/02259
	ation) DOCUMENTS CONSIDERED TO BE RELEVANT	
Category ²	Citation of document, with indication where appropriate, of the relevant passages	Relevant to claim No
A	STINE O.C. ET AL.: "Evidence for linkage of bipolar disorder to chromosome 18 with a parent-of-origin effect" AMERICAN JOURNAL OF HUMAN GENETICS. vol. 57, no. 6. 1995. pages 1384-1394. XP002087610 US cited in the application see the whole document	
А	MORS O. ET AL.: "Cytogenetic abnormalities on chromosome 18 associated with bipolar affective disorder or schizophrenia" BRITISH JOURNAL OF PSYCHIATRY, vol. 170, March 1997, pages 278-280, XP002087611 GB	
		i





International application No.

INTERNATIONAL SEARCH REPORT

	PCT/GB 98/02259
Box t Observations where certain claims were found unsearchable (Continu	ation of item 1 of first sheet)
This international Search Report has not been established in respect of certain claims under A	rticle 17(2)(a) for the following reasons.
Claims Nos.: because they relate to subject matter not required to be searched by this Authority, no	amely:
2. X Claims Nos.: CLAIMS 15, 16 pecause they relate to parts of the International Application that do not comply with the an extent that no meaningful International Search can be carried out, specifically: SEE FURTHER INFORMATION SHEET PCT/ISA/210	e prescribea requirements to sucn
3 Claims Nos because they are dependent claims and are not drafted in accordance with the secon	
Box II Observations where unity of invention is lacking (Continuation of item	2 of first sheet)
This International Searching Authority found multiple inventions in this international application	. as tollows
As all required additional search fees were timety paid by the applicant, this Internation searchable claims	nai Search Report covers aii

2	As all searchable claims could be searched without effort justifying an additional fee this Authority did not invite paymen of any additional fee
3	As only some of the required additional search fees were timely paid by the applicant, this international Search Report covers only those claims for which fees were paid, specifically claims Nos.
4	No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos

Remark on Protest The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/ GB 98 / 02259

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

CLAIMS NOS.: 15, 16

A search for the claims 15 and 16, respectively relating to a compound modulating the activity of the protein of claims 1 and 2 and to a substance modulating the compound identified by the method of claim 14, could not be performed, since the subject-matter is not sufficiently disclosed.



INTERNATIONAL SEARCH REPORT



information on patent family members

Internat | Application No | PCT/GB 98/02259

 					/ -4602	
Patent document cited in search report		Publication date		ratent family member(s)	Publication date	
WO 9737223	Α	09-10-1997	AU	26 5 9797 A	22-10-1997	



REQUEST

For recei	ffice use only
International Application No.	
International Filing Date	
Name of receiving Office and "	'PCT International Application"

The undersigned requests that the present international application be processed		14PCT I		
according to the Patent Cooperation Treaty.	Name of receiving Office and "PCT International Application"			
	Applicant's or agent's file reference (if desired) (12 characters maximum) PHM 70251/WO			
Box No. I TITLE OF INVENTION				
NOVEL COMPOUNDS				
Box No. II APPLICANT				
Name and address: (Family name followed by given name; for a legal entity, full official designation. The address must include postal code and name of country. The country of the address indicated in this Box is the applicant's State (that is, country) of residence is indicated below.) This person is also inventor. of residence is indicated below.)				
ZENECA Limited		Telephone No.		
15 Stanhope Gate		(01625) 516173		
London		Facsimile No.		
GB-W1Y 6LN	(01625) 583358			
GB				
		Teleprinter No. 669095/669388		
State (that is, country) of nationality: GB	State (that is, country)	of residence: GB		
This person is applicant for the purposes of: all designated X all designated X the United S		e United States the States indicated in the Supplemental Box		
Box No. III FURTHER APPLICANT(S) AND/OR (FURT	HER) INVENTOR(S)			
Name and address: (Family name followed by given name; for a designation. The address must include postal code and name of cou address indicated in this Box is the applicant's State (that is, country of residence is indicated below.) FLANNERY, Angela Veronica Alderley Park Macclesfield Cheshire GB-SK10 4TG GB	legal entity, full official ntry. The country of the v) of residence if no State	This person is: applicant only applicant and inventor inventor only (If this check-box is marked, do not fill in below.)		
State (that is, country) of nationality:	State (that is, country)			
GB		GB		
This person is applicant all designated all designate the United States		e United States the States indicated in the Supplemental Box		
Further applicants and/or (further) inventors are indicated on a continuation sheet.				
Box No. IV AGENT OR COMMON REPRESENTATIVE; OR ADDRESS FOR CORRESPONDENCE				
The person identified below is hereby/has been appointed to act of the applicant(s) before the competent International Authorities	on behalf X as:	gent common representative		
Name and address: (Family name followed by given name; for a designation. The address must include postal control of the contr	n legal entity, full official ode and name of country.)	Telephone No. (01625) 514304		
PHILLIPS, Neil Godfrey Alasdair				
Intellectual Property Department		Facsimile No.		
ZENECA Pharmaceuticals		(01625) 583358		
Mereside, Alderley Park		-,		
Macclesfield, Cheshire, GB-SK10 4TG, GB		Teleprinter No. 669095/669388		
Address for correspondence: Mark this check-box where space above is used instead to indicate a special address to				

Sheet No.

Continuation of Box No. III FUR PLICANT(S) AND/OR (FURTHER) INVENT					
If none of the following sub-boxes is used, this sheet should not be included in the request.					
Name and address: (Family name followed by given name; for a legal entity, full official designation. The address must include postal code and name of country. The country of the address indicated in this Box is the applicant's State (that is, country) of residence if no State of residence is indicated below.) FINNEGAN, Maria Christina Martina Alderley Park Macclesfield Cheshire GB-SK10 4TG GB	This person is: applicant only applicant and inventor inventor only (If this check-box is marked, do not fill in below.)				
State (that is, country) of nationality: IE State (that is, country) of nationality:					
This person is applicant all designated all designated States except the	United States				
for the purposes of: States the United States of America X of	America only the States indicated in the Supplemental Box				
Name and address: (Family name followed by given name; for a legal entity, full official designation. The address must include postal code and name of country. The country of the designation of the address indicated in this Box is the applicant's State (that is, country) of residence if no State of residence is indicated below.)	This person is: applicant only applicant and inventor inventor only (If this check-box is marked, do not fill in below.)				
State (that is, country) of nationality: State (that is, country) of	f residence:				
	United States the States indicated in the Supplemental Box				
Name and address: (Family name followed by given name; for a legal entity, full official designation. The address must include postal code and name of country. The country of the address indicated in this Box is the applicant's State (that is, country) of residence if no State of residence is indicated below.)	This person is: applicant only applicant and inventor inventor only (If this check-box is marked, do not fill in below.)				
State (that is, country) of nationality: State (that is, country) of	f residence:				
This person is applicant for the purposes of: all designated all designated States except the United States of America of America	United States America only the States indicated in the Supplemental Box				
Name and address: (Family name followed by given name; for a legal entity, full official designation. The address must include postal code and name of country. The country of the address indicated in this Box is the applicant's State (that is, country) of residence if no State of residence is indicated below.)	This person is: applicant only applicant and inventor inventor only (If this check-box is marked, do not fill in below.)				
State (that is, country) of nationality: State (that is, country) of	residence:				
	United States the States indicated in the Supplemental Box				
Further applicants and/or (further) inventors are indicated on another continuation she	et.				

Sheet No.

Box N	No.V	DESIGNATION OF STAILS	*		
The fo	ollowi	ng designations are hereby made under Rule 4.9(a) (n	ark t	he ap	plicable check-boxes; at least one must be marked).
Regional Patent					
ă		ZW Zilliozowe, and any other State which is a Conti	ractin	g Stai	no, MW Malawi, SD Sudan, SZ Swaziland, UG Uganda, te of the Harare Protocol and of the PCT
	EA	Eurasian Patent: AM Armenia A7 Azerbaijan	RV I	Relan	us, KG Kyrgyzstan, KZ Kazakhstan, MD Republic of nistan, and any other State which is a Contracting State
玆	EP	European Patent: AT Austria, BE Belgium, CH a DK Denmark, ES Spain, FI Finland, FR France, GB I	Juited	1 Kıns	itzerland and Liechtenstein, CY Cyprus, DE Germany, gdom, GR Greece, IE Ireland, IT Italy, LU Luxembourg, y other State which is a Contracting State of the European
Natio	nal Pa	itent (if other kind of protection or treatment desired,			
		Albania			Lesotho
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Precautionary Designation Statement: In addition to the designations made above, the applicant also makes under Rule 4.9(b) all other designations which would be permitted under the PCT except any designation(s) indicated in the Supplemental Box as being excluded from the scope of this statement. The applicant declares that those additional designations are subject to confirmation and that any designation which is not confirmed before the expiration of 15 months from the priority date is to be regarded as withdrawn by the applicant at the expiration of that time limit. (Confirmation of a designation consists of the filing of a notice specifying that designation and the payment of the designation and confirmation fees. Confirmation must reach the receiving Office within the 15-month time limit.)

Box No. VI PRIORITY CLAIM				Further priority claims are ated in the Supplemental Box.			
Filing date Number				Where earlier application is:			
of earlier application (day/month/year)	of earl	lier applicatio	on	national application: country	regional application:* regional Office		
item (1)	1 071			C.D.			
01 August 1997 (01.08.97)	9/10	6162.4		GB			
item (2)	1		\neg		 		
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The receiving Office is re of the earlier application purposes of the present in	(s) (only if nternational	the earlier a al application	applice i is the	ation was filed with the ereceiving Office) identif	Office which for the red above as item(s):	item (1)	
* Where the earlier application i Convention for the Protection of	s an ARIPO Industrial P	application, in	t is mo	andatory to indicate in the S	Supplemental Box at least (one country party to the Paris	
Box No. VII INTERNATI					tea (Rute 4.10(0)(11)). See	Зирріетепіаї вох.	
Choice of International Search	ching Auth	ority (ISA)	Reg	uest to use results of ear	lier search; reference	to that search (if an earlier	
(if two or more International Se competent to carry out the intern	earching Aut national sear	thorities are rch. indicate	searc	cn nas been carried out by oi	r requested from the Interne	ational Searching Authority):	
the Authority chosen; the two-let	ter code ma	y be used):	Date	(day/month/year)	Number	Country (or regional Office)	
ISA /							
Box No. VIII CHECK LIS	T; LANG	UAGE OF I	FILIN	1G			
This international application the following number of sheet	contains ets:	This interna		l application is accompar	nied by the item(s) mark	ed below:	
request :	4			igned power of attorney			
description (excluding sequence listing part) :	13			eneral power of attorney;	rafaranca number if an		
claims	3				•	y:	
abstract :	5 Santaning Lack of Signature						
drawings :	19		•	of international applicati	` '		
sequence listing part	16					r other biological material	
of description :				and/or amino acid seque		_	
Total number of sheets:	56	9. dother	r (spec	cify):		cadable form	
Figure of the drawings which should accompany the abstract	h :t:			nguage of filing of the mational application:	English		
Box No. IX SIGNATURE	OF APPL	JICANT OR	AGI	ENT			
Next to each signature, indicate the t					igns (if such capacity is not of	bvious from reading the request).	
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Neil Godfrey Alase	_ /						
AGENT	lair rn.	ILLI					
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international application:						2. Drawings:	
3. Corrected date of actual receipt due to later but timely received papers or drawings completing the purported international application:							
4. Date of timely receipt of the required corrections under PCT Article 11(2):						not received:	
International Searching Au (if two or more are competent)	ithority IS	SA /		6. Transmitt until searce	al of search copy delaye ch fee is paid.	ed	
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Date of receipt of the record copy by the International Bureau:							



INTERNATIONAL SEARCH REPORT

(PCT Article 18 and Rules 43 and 44)

Applicant's or agent's file reference	1 (Form PCT/ISA/2	f Transmittal of International Search Report 20) as well as, where applicable, item 5 below.						
PHM 70251/W0	ACTION							
International application No.	International filing date (day/month/year)	(Earliest) Priority Date (day/month/year)						
PCT/GB 98/02259	28/07/1998	01/08/1997						
Applicant								
ZENECA LIMITED et al.								
This International Search Report has been prepared by this International Searching Authority and is transmitted to the applicant according to Article 18. A copy is being transmitted to the International Bureau.								
This International Search Report consists It is also accompanied by a cop	of atotal of5sheets. y of each priorant document cited in this report.							
1. X Certain claims were found un	searchable(see Box I).							
2. Unity of invention is lacking(s	see Box II).							
	ntains disclosure of a nucleotide and/or amin dout on the basis of the sequence listing	o acid sequence listing and the						
filed with the international application.								
furnished by the applicant separately from the international application.								
	but not accompanied by a statement to the matter going beyond the disclosure in the							
Tra	nscribed by this Authority							
4. With regard to the title , the	text is approved as submitted by the applicant							
X the	text has been established by this Authority to re	ead as follows:						
ZGGBP1, NOVEL PEPTIDE AND USES THEREOF	S RELATED TO BIPOLAR AFFECT	IVE DISORDER TYPE 1, SEQUENCES						
5. With regard to the abstract,								
X the	text is approved as submitted by the applicant							
Box	text has been established, according to Rule 3 ctll. The applicant may, within one month from arch Report, submit comments to this Authority	the date of mailing of this International						
6. The figure of the drawings to be pub	lished with the abstract is.	_						
	suggested by the applicant.	X None of the figures						
=	cause the applicant failed to suggest a figure.							
bec	cause this figure better characterizes the invent	on.						



Box I Observations where certain claims	were found unsearchable (Continuation of Item 1 of first sheet)
This International Search Report has not been esta	blished in respect of certain claims under Article 17(2)(a) for the following reasons:
Claims Nos.: because they relate to subject matter not.	required to be searched by this Authority, namely:
2. X Claims Nos.: CLAIMS 15 because they relate to parts of the International an extent that no meaningful International SEE FURTHER INFORMATION S	tional Application that do not comply with the prescribed requirements to such Search can be carried out, specifically:
3. Claims Nos.: because they are dependent claims and a	are not drafted in accordance with the second and third sentences of Rule $6.4(a)$.
Box II Observations where unity of inven	tion is lacking(Continuation of item 2 of first sheet)
This International Searching Authority found multiple	e inventions in this international application. as follows:
As all required additional search fees were searchable claims.	e timely paid by the applicant, this International Search Report covers all
2. As all searchable claims could be searche of any additional fee.	ed without effort justifying an additional fee, this Authority did not invitepayment
As only some of the required additional secovers only those claims for which fees w	earch fees were timely paid by the applicant, this International Search Report ere paid, specifically claims Nos.:
No required additional search fees were ti restricted to the invention first mentioned	mely paid by the applicant. Consequently, this International Search Report is in the claims: it is covered by claims Nos.:
Remark on Protest	The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.

International Application No. PCT/ GB 98 / 02259

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

CLAIMS NOS.: 15, 16

A search for the claims 15 and 16, respectively relating to a compound modulating the activity of the protein of claims 1 and 2 and to a substance modulating the compound identified by the method of claim 14, could not be performed, since the subject-matter is not sufficiently disclosed.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Claims Nos.: 15 16

A search for the claims 15 and 16, respectively relating to a compound modulating the activity of the protein of claims 1 and 2 and to a substance modulating the the compound identified by the method of claim 14, could not be performed, since the subject-matter is not sufficiently disclosed.

A. CLASSIFICATION OF SUBJECT MATTER IPC 6 C12N15/00 C07K14/435

C12N9/10

C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

 $\begin{array}{ccc} \text{Minimum documentation searched} & \text{(ciassification system followed by classification symbols)} \\ IPC & 6 & C07K & C12N \\ \end{array}$

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

Category ^c	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No
Х,Р	WO 97 37223 A (UNIV NORTH CAROLINA) 9 October 1997	6,10, 12-14, 18-21
А	see abstract see page 9, line 1 - page 10, line 23 see figure 23 see claim 48 see Nos.125 and 126 of Sequence Listing	1,2,4
X , P	OHARA O. ET AL.: "Prediction of the sequences of unidentified human genes. VIII. The complete senquences of 77 new cDNA clones from brain which can code for large proteins in vitro" EMBL DATABASE,5 December 1997, XP002087609 HEIDELBERG, DE AC: AB007899	1,2,4, 8-10,18, 21

X Further documents are listed in the continuation of box C.	χ Patent family members are listed in annex.
 Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filling date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P document published prior to the international filing date but later than the priority date claimed 	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention. "X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone." "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art. "&" document member of the same patent family
Date of the actual completion of the international search 11 December 1998	Date of mailing of the international search report $12/01/1999$
Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Te' (+31-70) 340-2040, Tx. 31 651 epo nl. Fax. (+31-70) 340-3016	Panzica, G

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PC 98/02259

		96/02259
	ation) DOCUMENTS CONSIDERED TO BE RELEVANT	
Category ¹	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No
A	STINE O.C. ET AL.: "Evidence for linkage of bipolar disorder to chromosome 18 with a parent-of-origin effect" AMERICAN JOURNAL OF HUMAN GENETICS, vol. 57, no. 6, 1995, pages 1384-1394, XP002087610 US cited in the application see the whole document	
A	MORS O. ET AL.: "Cytogenetic abnormalities on chromosome 18 associated with bipolar affective disorder or schizophrenia" BRITISH JOURNAL OF PSYCHIATRY, vol. 170, March 1997, pages 278-280, XP002087611 GB	

1



PC 98/02259

Patent document cited in search report Publication date Patent family member(s) Publication date

WO 9737223 A 09-10-1997 AU 2659797 A 22-10-1997



PCT

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

(PCT Article 36 and Rule 70)

PHM 702		nt's file reference	FOR FURTHER AC	See Note TION Prelimina	fication of Transmittal of International ary Examination Report (Form PCT/IPEA/416)
Internationa			International filing date (day/month/year)	Priority date (day/month/year)
PCT/GB9			28/07/1998		01/08/1997
International C12N15/		nt Classification (IPC) or	national classification and IPC	2	
Applicant					
ZENECA	LIM	TED et al.			
and is	trans	smitted to the applicar	nt according to Article 36.		nternational Preliminary Examining Authority
2. This F	REPC	RT consists of a total	of 8 sheets, including this	s cover sheet.	
b (s	een a see R	mended and are the l	pasis for this report and/or a 607 of the Administrative	sheets containing	tion, claims and/or drawings which have rectifications made before this Authority the PCT).
3. This r	eport	contains indications r	elating to the following iter	ms:	
1	ß	Basis of the report			
11		Priority			
111		•	of opinion with regard to no	ovelty, inventive st	ep and industrial applicability
IV		Lack of unity of inve			
٧	ß		t under Article 35(2) with re ations suporting such state		nventive step or industrial applicability;
VI	[]	Certain documents	cited		
VII		Certain defects in th	e international application		
VIII	⊠	Certain observations	s on the international appli	cation	
Date of sub	missi	on of the demand		Date of completion	of this report
08/02/19	99				0 3. 11. 99
		g address of the internati	onal	Authorized officer	Control of Color

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Form PCT/IPEA/409 (cover sheet) (January 1994)

European Patent Office D-80298 Munich

Tel +49 89 2399 - 0 Tx 523656 epmu d

International application No. PCT/GB98/02259

I. Basis of the report

1. This report has been drawn on the basis of (substitute sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to the report since they do not contain amendments.):

	the	report since they d	o not contain amendments.):
	Des	scription, pages:	
	1-13	3	as originally filed
	Cla	ims, No.:	
	1-2	1	as originally filed
	Dra	wings, sheets:	
	1/19	9-19/19	as originally filed
2.	The	amendments have	e resulted in the cancellation of:
		the description,	pages:
		the claims,	Nos.:
		the drawings,	sheets:
3.			een established as if (some of) the amendments had not been made, since they have been beyond the disclosure as filed (Rule 70.2(c)):
4.	Add	ditional observation	s, if necessary:
11.	Prie	ority	
1.		This report has be prescribed time lin	een established as if no priority had been claimed due to the failure to fumish within the nit the requested:
		□ copy of the ea	arlier application whose priority has been claimed.
		☐ translation of	the earlier application whose priority has been claimed.
2.		This report has be	een established as if no priority had been claimed due to the fact that the priority claim has

International application No. PCT/GB98/02259

Thus for the purposes of this report, the international filing date indicated above is considered to be the relevant date.

	or the purposes of the report and more many and the second						
3. A d	ditional observations, if necessary:						
se	e separate sheet						
II. No	on-establishment of opinion with regard to novelty, inventive step and industrial applicability						
	juestions whether the claimed invention appears to be novel, to involve an inventive step (to be non-obvious), be industrially applicable have not been examined in respect of:						
	the entire international application.						
\boxtimes	claims Nos. 14,15, 16.						
ecau	use:						
	the said international application, or the said claims Nos. relate to the following subject matter which does not require an international preliminary examination (<i>specify</i>):						
	the description, claims or drawings (indicate particular elements below) or said claims Nos. are so unclear that no meaningful opinion could be formed (specify):						
\boxtimes	the claims, or said claims Nos. 14 are so inadequately supported by the description that no meaningful opinion could be formed.						
\boxtimes	no international search report has been established for the said claims Nos. 15, 16.						

International application No. PCT/GB98/02259

V. Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

1. Statement

Novelty (N)

Yes:

Claims 3, 12, 13, 17-20

No:

Claims 1, 2, 4-11, 21

Inventive step (IS)

Yes:

Claims none

No:

Claims 1-13, 17-21

Industrial applicability (IA)

Yes:

Claims 1-13, 17, 18, 20, 21

No:

Claims 19 (reserved opinion)

2. Citations and explanations

see separate sheet

VI. Certain documents cited

1. Certain published documents (Rule 70.10)

and / or

2. Non-written disclosures (Rule 70.9)

see separate sheet

VIII. Certain observations on the international application

The following observations on the clarity of the claims, description, and drawings or on the question whether the claims are fully supported by the description, are made:

see separate sheet

II. PRIORITY

This first preliminary written opinion has been established considering the priority 1) date 01.08.97 as a valid date. The Applicant is reminded that documents: WO 97 37223 A (UNIV NORTH CAROLINA) 9 October 1997 OHARA O. ET AL. in EMBL DATABASE, 5 December 1997 cited in the international search report may become relevant after consideration of the priority document which is unavailable at present.

III. NON-ESTABLISHMENT OF OPINION

- The subject-matter of Claim 14 is not supported by the description and thus, it is 2) not amenable to examination of novelty, inventive step or industrial applicability. Said claim relates to a method for identifying a compound capable of modulating the activity of a ZGGBP1 protein. However, a function of said protein has not been demonstrated. Sequence analysis of the encoding gene has revealed several structural domains which correspond to several potential functions (p. 2). Furthermore, sequence homology of the encoding gene with at least two different genes, nedd-4 and Pub3, indicates even more potential functions (p.3). The application as filed, does not provide any indication as to which of all the potential activities of ZGGBP1 the method of Claim 14 is directed to. Since the method of said claim is not supported by the description, an opinion cannot be established.
- No opinion is established for the subject-matter of Claims 15 and 16 because 3) said claims relate to inventions in respect of which no international search report has been established (Rule 66.1(e) PCT).

V. REASONED STATEMENT UNDER ARTICLE 35(2)

The present application relates to the isolation of a cDNA clone comprising the 4) sequence presented in SEQ ID NO1, called gene ZGGBP1. Said sequence resides, along with many other expressed sequences, in the 18q21 chromosomal region which was shown previously to be associated with the neurological disorder bipolar affective disorder. The ZGGBP1 gene sequence appears to have 85% identity at the amino acid level with the human gene encoding nedd-4 which

was shown previously to be a negative regulator of a sodium channel which is deleted in Liddle's syndrome (a hereditary form of hypertension). The ZGGBP1 gene sequence shares also 100% identity, over a 3kb region, with the previously identified gene, Pub3 which may be involved in regulation of cell cycle of eukaryotic cells. The Applicant has not demonstrated that said ZGGBP1 gene has any function.

The subject-matter of Claims 1, 2, 4-11, 21 is not novel as required by Article 5) 33(2) PCT.

Claim 1 relates to a polynucleotide comprising a nucleic acid sequence encoding the polypeptide of SEQ ID NO 2, and homologues and fragments.

Figure 2 of the present application discloses the amino acid sequence of the known human nedd-4 gene which is 85% homologous to polypeptide of SEQ ID NO 2 (p.11). Figure 5 of the present application discloses the nucleotide sequence of the known gene Pub-3 which comprises fragments up to 3 kb long which are identical to the polynucleotide encoding SEQ ID NO 2.

Thus, the subject-matter of said claim has been disclosed in the prior art.

Similar arguments apply for the subject-matter of Claims 2, 4-11, 21.

The subject-matter of Claims 3, 12, 13, 17-20 is not inventive as required by 6) Article 33(3) PCT.

Said claims refer to subject-matter as defined in Claims 1-7, 10 or 11 and comprise additional technical features which may render said subject-matter novel. However, said technical features represent standard options available to the skilled person aware of the state of the art in the field of gene technology. Thus, said technical features do not impart any inventiveness to said subjectmatter. Consequently, even if it is assumed that the subject-matter of Claims 3, 12, 13, 17-20 is novel, said claims do not comprise an inventive step.

Claim 19 is directed to the use of a polynucleotide in gene therapy. Said claim is 7)

EXAMINATION REPORT - SEPARATE SHEET

thus, considered to be directed to method of treatment of the human or animal body. For the assessment of claims as far as they are directed to a method of treatment of the human or animal body or to a diagnostic method practised on the human or animal body, no unified criteria exist in the PCT, on the question whether they are industrially applicable. The patentability can be dependent upon the formulation of the claims.

VI. CERTAIN DOCUMENTS CITED

The following documents are cited under Rule 70.10 PCT 8) WO 97 37223 A, 9.10.97, filed 03.04.97, with priority date of 03.04.96

VIII. CERTAIN OBSERVATIONS ON THE INTERNATIONAL APPLICATION

- The Applicant is reminded that the claims must be comprehensible from the 9) technical point of view and clearly define the object of the invention, that is to say indicate all the essential features thereof (Rule 6 PCT). The subject-matter of Claims 3, 7, 17 and 21 does not fulfil this condition, as the claimed nucleic acid is only defined by the name of the encoded protein "ZGGBP1" without disclosing any technical feature which unambiguously characterizes the claimed subjectmatter. A gene being a chemical product should be clearly defined by its formula i.e. its nucleotide sequence.
- 10) Claim 1 is drafted towards an isolated nucleic acid with specified sequence content. However, the function of said nucleic acid is not clearly stated in the claim.

The Applicant speculates in the description that said nucleic acid encodes a protein which may be associated with the bipolar affective disorder although no evidence for such association is presented. Furthermore, even if such an association of the claimed protein with the bipolar affective disorder is established, a function of the protein is not defined nor could be speculated, especially since sequence analysis of the protein appears to indicate several potential functions. Since there is no conclusive demonstration of any function of the polypeptide of SEQ ID NO 2, as such, any function can, at best, be accepted as speculative. At

this point, it is not apparent what problem said polypeptide or fragments thereof are intended to solve or whether said sequences represent a solution comprising an inventive step. Insufficient disclosure of essential technical features, such as the function of a given nucleotide or amino acid sequence, does not allow for the acknowledgement of an inventive step involved in solving a technical problem. The lack of sufficient disclosure of the invention is contrary to Article 5 PCT and makes it difficult if not impossible to examine the novelty and inventive step of the claimed invention.

The same arguments apply to the subject-matter of Claims 2-7 and 10-12.

11) The subject-matter of Claim 11 is not clear as required by Rule 6 PCT. Said claim relates to a polypeptide comprising the amino acid sequence of SEQ ID NO 4. As said sequence is being disclosed only in the sequence listing without any mention of it in the description, it is not entirely clear what relation it bears with the invention as disclosed in the present application.

. "ENT COOPERATION TREAT"

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01 April 1999 (01.04.99)	in its capacity as elected Office					
International application No.	Applicant's or agent's file reference					
PCT/GB98/02259	PHM 70251/WO					
International filing date (day/month/year)	Priority date (day/month/year)					
28 July 1998 (28.07.98)	01 August 1997 (01.08.97)					
Applicant						
FLANNERY, Angela, Veronica et al						
The designated Office is hereby notified of its election made						
X in the demand filed with the International Preliminary	Examining Authority on:					
08 February 19	99 (08.02.99)					
in a notice effecting later election filed with the International Bureau on:						
2. The election X was						
was not						
made before the expiration of 19 months from the priority of Rule 32.2(b).	late or, where Rule 32 applies, within the time limit under					
Nule 32.2(b).						
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C. Carrié

Telephone No.: (41-22) 338.83 38



WORLD INTELLECTUAL PROPERTY ORGANIZATION International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ :		(11) International Publication Number: WO 99/06539
C12N 15/00, C07K 14/435, C12N 9/10, C12Q 1/68	A1	(43) International Publication Date: 11 February 1999 (11.02.99)
(21) International Application Number: PCT GBS (22) International Filing Date: 28 July 1998 (2)		DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT,
 (30) Priority Data: 9716162.4 1 August 1997 (01.08.97) (71) Applicant (for all designated States except US): Z LIMITED [GB/GB]: 15 Stanhope Gate, London W (GB). (72) Inventors; and (75) Inventors/Applicants (for US only): FLANNERY, Veronica [GB/GB]; Alderley Park, Macclesfield, SK10 4TG (GB). FINNEGAN, Maria, Christina, [IE/GB]; Alderley Park, Macclesfield, Cheshire SK (GB). (74) Agent: PHILLIPS, Neil, Godfrey, Alasdair; Zeneca Phaticals, Intellectual Property Dept., Mereside, Alderley Macclesfield, Cheshire SK10 4TG (GB). 	ZENEC 'IY 6L Angel Cheshi Martii K10 4T	N a, tree ha G
(54) Title: ZGGBP1, NOVEL PEPTIDES RELATED TO THEREOF	O BIPO	DLAR AFFECTIVE DISORDER TYPE 1. SEQUENCES AND USES

(57) Abstract

A new human gene (ZGGBP1) is described which is associated with neurological affective disorders such as bipolar affective disorder. A full-length cDNA encoding human ZGGBP1 and a partial cDNA encoding muringe ZGGBP1 are disclosed. Polymorphic variants of the gene and functional domains encoded within the gene are also provided. The invention further relates to methods for identifying compounds which modulate the activity of ZGGBP1 protein, and to diagnostic assays for the detection of ZGGBP1 in biological samples.

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ZGGBP1, NOVEL PEPTIDES RELATED TO BIPOLAR AFFECTIVE DISORDER TYPE 1, SEQUENCES AND USES THEREOF

This invention relates to a novel human gene (ZGGBP1) associated with affective neurological disorders such as bipolar affective disorder. The invention also relates to homologues of the ZGGBP1 gene in species such as rat and mouse useful in providing animal models of affective disorders. The invention further relates to both the cDNA and the structural gene and to fragments encoding functional domains within the gene. The invention also relates to means for producing the protein encoded by the gene and to means for regulating its production and activity in vivo.

Affective disorders comprise a broad and heterogeneous category of psychiatric illness with a prevalence of up to 20% in the population. The most severe of these disorders is bipolar type I which affects approximately 1% of the population and this rate is fairly consistent across countries. The disease affects young adults, with a mean age of onset of 22 years. Treatment depends upon the phase of the disease and pharmacological agents include lithium carbonate, carbamazepine or valproic acid, tricyclic antidepressants. Monoamine oxidase inhibitors and selective serotonin re-uptake inhibitors are now also being used. The success rate of individual drugs is variable and some patients are treated with a combination of agents, although most have some unwanted side-effects. At present the precise diagnosis of individual affective disorders is difficult and new, gene based, diagnostic methods are desirable.

Family, twin and adoption studies have suggested the importance of genetic predisposition to bipolar affective disorder. On this basis, several groups have undertaken genetic linkage analysis in families with a high incidence of the disorder to find a causal gene. Many of the studies show conflicting data suggesting that a single gene is unlikely to be the cause. Rather, multiple interacting genetic traits may be involved. A recent study (Stine et al. 1995) identified two regions on chromosome 18 showing linkage to the disease.

The present invention is based on our discovery of a novel gene which maps to 18q21 and which unexpectedly shows appreciable sequence homology to the ned-4 gene on chromosome 15. Ned-4 is the human homologue of the mouse nedd-4 gene which is known to be differentially expressed during neural development and to be involved in signal transduction. Human ned-4 has been shown (Schild et al. 1996, Straub

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et al. 1996) to be a negative regulator of a sodium channel which is deleted in Liddle's syndrome (a hereditary form of hypertension).

Nedd-4 was originally isolated as a partial cDNA clone from a mouse brain library (Kumar et al. 1992) as one of a set of genes which were differentially expressed during development (Neural precursor cells expressed developmentally down-regulated). The derived amino acid sequence contains three copies of the WW domain (Andre & Springael 1994, Bork & Sudol, 1994; Hofmann & Boucher, 1995), a Ca lipid binding (CaLB/C2) domain (Brose et al. 1995) and a Hect (homologous to the E6-AP carbodyl terminus) domain which has homology to a ubiquitin ligase (E3) enzyme (Huibregtse et al. 1995). The human homologue of nedd-4 (Ned-4) was isolated as an randomly cloned EST (K1AA0093) from immature myeloblast mRNA (Nomura et al. 1994) and shown by sequence comparison to have 86% identity at the amino acid level to the mouse sequence. The human sequence, however, has a fourth copy of the WW domain.

The WW domain is a 40 amino acid sequence found in several unrelated proteins. The two highly conserved tryptophans give it its name. The function of the domain is thought to be involved in protein-protein interactions. Despite their functional diversity, the proteins listed all appear to be involved in cell signalling or regulation. It has been shown that the WW domains of Nedd-4 interact with the proline-rich PY motifs in the epithelial sodium channel in the kidney (Schild et al. 1996). Mutational deletion of the PY motifs in the epithelium sodium channel in Liddle's syndrome, an inherited disease causing systemic hypertension characterised by hyperactivity of the sodium channel, has been shown to abrogate binding of Nedd-4 (Straub et al. 1996). It is therefore likely that Nedd-4 has a negative regulatory role when bound to the channel.

The Hect domain is an E3 ubiquitin-protein ligase domain and enzymes with this domain catalyse polyubiquitination, which is involved in several cellular processes including proteolytic degradation.

The CaLB/C2 domain is thought to be involved in calcium-dependent phospholipid binding, although some proteins containing this domain do not bind calcium and other putative functions for the C2 domain such as binding to inositol -1,3,4,5-tetraphosphate have been suggested. Examples of proteins containing this domain are Protein Kinase C (PKC) isoenzymes and synaptogamins.

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PCT patent application WO97/12962 discloses a protein (Pub3) with homology to Pub1, a Schizosaccaromyces Pombe protein which has an apparent function in the ubiquitination of, among other cellular proteins, the mitotic activating tyrosine phosphatase cdc25 and the tumour suppresser protein p53. As such this protein may be involved in regulating the progression of proliferation in eukaryotic cells by effectively controlling the activity of the cdk complexes by modulating the availability of cdc25 and/or p53.

A comparison of Pub3 with ZGGBP1 revealed that the sequences represent two distinct genes which code for two separate, structurally unrelated proteins. The two genes share sequence homology within a certain defined region, the sequences are identical within the region 516-3568 of ZGGBP1, but they do not show any homology within the regions 5' and 3'of this sequence. In addition the derived amino acid sequence for ZGGBP1 is completely different to that derived for Pub 3 as both have been initiated from a different start methionine. A comparison of the nucleotide sequences for ZGGBP1 and Pub 3 is outlined in Figure 5.

Therefore in a first aspect of the present invention we provide the ZGGBP1 gene having the full length cDNA as set out in SEQ ID NO: 1. We further provide fragments of the ZGGBP1 gene comprising ZGGBP1 sequence outside the region defined by base pairs 516-3568 of the ZGGBP1 gene. By fragments we mean contiguous regions of the gene including complementary DNA and RNA sequences, starting with short sequences useful as probes or primers of say about 8-50 bases, such as 10-30 bases or 15-35 bases, to longer sequences of up to 50, 100, 200, 500 or 1000 bases. Indeed any convenient fragment of the gene of say up to 2kb, 3kb, 4kb or more than 4kb may be a useful gene fragment for further research, therapeutic or diagnostic purposes. Further convenient fragments include those whose terminii are defined by restriction sites within the gene of one or more kinds, such as any combination of Rsa1, Alu1 and Hinf1.

In a further aspect of the invention we provide homologues of the ZGGBP1 gene in species such as rat and mouse useful in providing animal models of affective disorders. By homologue, we mean a corresponding ZGGBP1 gene in another species, which displays greater than 85% sequence homology, conveniently greater than 90%, for example 95%, to the human ZGGBP1 sequence. The full sequences of the individual homologues may be determined using conventional techniques such as hybridisation, PCR

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and sequencing techniques, starting with any convenient part of the sequence set out in SEQ ID NO: 1. The partial sequence of the mouse gene is set out in SEQ ID NO: 3 and this gene and the protein encoded by this gene represent further independent aspects of the invention.

In a further aspect of the invention we provide polynucleotide sequences capable of specifically hybridising to the ZGGBP1 gene. By specifically hybridising we mean that the polynucleotide hybridises under stringent conditions to the sequence on chromosome 18q21 as set out in SEQ ID No: 1, or to the corresponding non-coding sequence, to the exclusion of other genomic loci. It is contemplated that a species such as a peptide nucleic acid may be an acceptable equivalent to a polynucleotide, at least for purposes that do not require translation into protein.

In a further aspect of the invention we provide a recombinant ZGGBP1 protein obtained by expression of all or a part of the cDNA as set out in SEQ ID NO: 1. The recombinant protein may comprise all or a convenient part of the peptide sequence set out in SEQ ID NO: 2. The production of a protein according to the invention may be achieved using standard recombinant DNA techniques involving the expression of the protein by a host cell as described for example by Sambrook et al. 1989. The isolated nucleic acids described herein may for example be introduced into any convenient expression vector—for example the T7 Studier system for expression in E.coli (US-A-4952496), Pichia pastoris for expression in yeast, the Baculovirus system for expression in insect cells and the GS system for expression in mammalian cells by operatively linking the DNA to any necessary expression control elements therein and transforming any suitable—prokaryotic or eukaryotic host cell with the vector using well known procedures.

Therefore in a further aspect of the invention we provide a recombinant plasmid comprising all or a part of the ZGGBP1 cDNA of the invention.

The invention further extends to cells containing said recombinant plasmids and to a process for producing a ZGGBP1 protein of the invention which comprises culturing said cells such that the desired protein is expressed and recovering the protein from the culture.

By way of example, the nucleotide sequence in SEQ ID NO: 1 is inserted downstream of the SV40 promoter in the pGEX plasmid vector, and either transiently or

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stably expressed in COS -7 cells. Expression of the protein according to the invention can be detected following disruption of the cells by Western blotting.

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It may be desirable to produce the individual functional domains of the protein according to the invention in isolation from the rest of the molecule. This may be achieved using the above standard recombination DNA techniques except that in this instance the DNA sequence used is that encoding one of the partial amino acid sequences of the domains identified in Figure 1 or a combination of these.

By way of further example, the nucleotide sequence in SEQ ID NO: 1 is inserted downstream of the SV40 promoter and the glutathione-S-transferase (GST) coding sequence in the pBC plasmid vector, and either transiently or stably expressed in COS -7 cells allowing expression of the corresponding fusion protein. Expression of the fusion protein can be detected following disruption of the cells by Western blotting with antibodies to GST, and furthermore the fusion protein can be used in an affinity binding procedure to find proteins which are functional partners of the protein of the invention from cell extracts.

A ZGGBP1 protein of the invention may in particular be used to screen for compounds which regulate the activity of the enzymes and the invention extends to such a screen and to the use of compounds obtainable therefrom to regulate the activity of the protein in vivo.

Thus according to a further aspect of the invention we provide a method for identifying a compound capable of modulating the action of a ZGGBP1 protein which method comprises subjecting one or more test compounds to a screen comprising (A) a protein containing the amino acid sequence shown in SEQ ID NO: 2 or a homologue or fragment thereof, or (B) the nucleotide sequence shown in SEQ ID NO: 1 or a homologue or fragment thereof, or (C) a host cell expressing a ZGGBP1 polypeptide or a homologue or fragment thereof.

The screen according to the invention may be operated using conventional procedures, for example by bringing the test compound or compounds to be screened and an appropriate substrate into contact with the protein or a cell capable of producing it and determining affinity for the protein in accordance with conventional procedures.

Any compound identified in this way may be used in the treatment of humans and/or other animals of one or more of the above mentioned diseases. The invention thus

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extends to a compound selected through its ability to regulate the activity of the protein in vivo as primarily determined in a screening assay utilising the protein containing an amino acid sequence shown in SEQ ID NO: 2 or a homologue or fragment thereof, or a gene coding therefor for use in the treatment of a disease in which the over- or under-activity or unregulated activity of the protein is implicated.

In a further aspect of the invention we provide examples of insertions/deletions and single base change polymorphisms (mutations) as outlined in Figure 6, 7, 8, 9 and 10.

The ZGGBP1 gene of the invention may also be used as the basis for diagnosis, for example to determine expression levels in a human subject, by for example direct DNA sequence comparison or DNA/RNA hybridisation assays. Diagnostic assays may involve the use of nucleic acid amplification technology such as the PCR and in particular the Amplification Refractory Mutation System (ARMS) as claimed in our European Patent No. 0 332 435. Such assays may be used to determine allelic variants of the gene, for example insertions, deletions and/or mutations such as one or more point mutations. Such variants may be heterozygous or homozygous.

In a further aspect of the invention, amplification primers may be provided for use in the above diagnostic methods. In general, these are provided as a set and used for PCR amplification. One of the primers conveniently hybridises to a ZGGBP1 locus outside the region defined by base pairs 516-3568 thus allowing the ZGGBP1 gene on 18q21 to be identified to the exclusion of other loci.

The ZGGBP1 gene may also be used in gene therapy, for example where it is desired to modify the production of the protein in vivo, and the invention extends to such uses.

Knowledge of the gene according to the invention also provides the ability to regulate its expression in vivo by for example the use of antisense DNA or RNA. Thus, according to a further aspect of the invention we provide an antisense DNA or an antisense RNA which is complementary to the polynucleotide sequence shown in SEQ ID NO: 1. By complementary we mean that the two molecules can base pair to form a double stranded molecule.

The antisense DNA or RNA for co-operation with the gene in SEQ ID NO: 1 can be produced using conventional means, by standard molecular biology and/or by chemical synthesis as described above. If desired, the antisense DNA or antisense RNA may be

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chemically modified so as to prevent degradation in vivo or to facilitate passage through a cell membrane and/or a substance capable of inactivating mRNA, for example ribozyme, may be linked thereto and the invention extends to such constructs.

The antisense DNA or antisense RNA may be of use in the treatment of diseases or disorders in humans in which the over- or under-regulated production of the gene product has been implicated. Such diseases or disorders may include those described under the general headings of neurologic, eg.stroke, dementia, renal eg. hypertension, nephrosis, cardiovascular disorders.

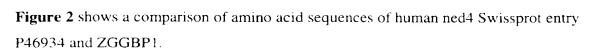
Convenient DNA sequences may be obtained using conventional molecular biology procedures, for example by probing a human genomic or cDNA library with one or more labelled oligonucleotide probes containing 10 or more contiguous nucleotides designed using the nucleotide sequences described here. Alternatively, pairs of oligonucleotides one of which is homologous to the sense strand and one to the antisense strand, designed using the nucleotide sequences described here to flank a specific region of DNA may be used to amplify that DNA from a cDNA library.

The ZGGBP1 protein of the invention and homologues or fragments thereof may be used to generate substances which selectively bind to it and in so doing regulate the activity of the protein. Such substances include, for example, antibodies, and the invention extends in particular to an antibody which is capable of recognising one or more epitopes containing the protein binding domains shown in Figure 1. In particular the antibody may be neutralising antibody.

As used herein the term antibody is to be understood to mean a whole antibody or a fragment thereof, for example a F(ab)2, Fab, FV,. VH or VK fragment, a single chain antibody, a multimeric monospecific antibody or fragment thereof, or a bi- or multispecific antibody or fragment thereof.

The invention will now be illustrated but not limited by reference to the following detailed description, References, Examples and Figures wherein:

Figure 1 shows the predicted amino acid sequence of ZGGBP1. The C2 domain is indicated by carets, the four WW domains are indicated by asterisks, and the Hect domain is indicated by underlining.



- Figure 3 shows a Northern blot analysis of various human tissues probed with ZGGBP1.
- Figure 4 shows a comparison of the nucleic acid sequences of human and mouse
- 5 ZZGBP1. The mouse sequence is a partial cDNA which spans the C-terminal portion of the human protein coding region.
 - Figure 5 shows a comparison of the nucleic acid sequences for ZGGBP1 and Pub3
 - Figure 6 shows a polymorphism located at position 3554 of the cDNA sequence
 - Figure 7 shows a polymorphism located at position 4828 of the cDNA sequence
- Figure 8 shows a polymorphism located in an intronic sequence derived from a BAC containing ZGGBP1
 - **Figure 9** shows a variable number of tetranucleotide repeats located within an intronic sequence from ZGGBP1
 - Figure 10 shows an insertion at position 4032 of the cDNA sequence

References

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Stine O.C. et al. (1994) Am.J.Hum.Genet. 57, 1384-1394;

Lovett M., Kere J. and Hinton L. (1991) Proc.Natl.Acad.Sci. USA 88, 9628-9632;

Schuler G.D. et al. (1996) Science 274, 540-546;

20 Kumar S., Tomooka Y. and Noda M. (1992) Biochem.Biophys.Res.Commun. 185, 1155-1161;

Andre B. and Springael J.Y. (1994) Biochem.Biophys.Res.Commun. 205, 1201-1205;

Bork P. and Sudol M. (1994) Trends Biochem.Sci. 19, 531-533;

Hofmann K. and Boucher P. (1995) FEBS Letts. 358, 153-157;

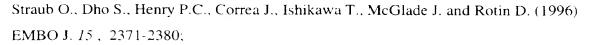
25 Brose N., Hofmann K.O., Hata Y., Suedhof T.C.(1995) J. Biol. Chem. *270*, 25273-25280;

Huibregtse J.M., Scheffner M., Beaudenon S. and Howley P.M. (1995)

Proc.Natl.Acad.Sci. USA, 92, 2563-2567;

Nomura N. et al. (1994) DNA Res. 2, 37-43;

Schild L., Lu Y., Gautschi I., Schneeberger E., Lifton R.P. and Rossier B.C. (1996) EMBO J. 15, 2381-2387;



Shizua H., Birren B., Kim U-J, Mancino V., Slepak T., Tachiiri Y. and Simon M. (1992) Proc.Natl.Acad.Sci. USA 89, 8794-8797;

5 Kim U-J., Shizuya H., Kang H-L., Choi S-S., Garrett C.L., Smink L.J., Birren B.W., Korenberg J.R., Dunham I. and Simon M. (1996) Proc.Natl.Acad.Sci. USA 93, 6297-6301.

Sambrook J., Fritsch E.F. and Maniatis T. (1989) "Molecular Cloning: A Laboratory Manual (2nd edition)" Cold Spring Harbor Laboratory Press NY

Example 1

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Identification of ZGGBP1

We used two methods for investigating the 18q21 region of interest. In one method we used positional cloning to identify novel transcripts from physical clones representing the region and in a second method we utilised public databases to identify transcripts which had been assigned to a low resolution map of the region by radiation hybrid mapping and assigned them to physical clones representing a high resolution map of the region.

20 **Method 1 - Positional Cloning**

The 18q21 region described by Stine et al. (1995) is delimited by the STS markers used by that group to identify linkage. They found the most strongly linked marker to be D18S41, which had a LOD score of 3.51 in cases of paternal inheritance. Linkage declined over flanking markers. We identified a set of four Yeast Artificial Chromosomes (YACs) which comprised a contiguous overlapping set of genomic clones covering the defined region by the presence in those YACs of STS markers used in the Stine study.

DNA from the YACs was prepared and used in a PCR-based hybridisation approach to enrich for transcripts from a human fetal brain cDNA library. This approach, known as direct selection (Lovett et al. 1991) has been shown to be efficient in identifying transcripts present on large genomic clones.

Method 2 - Refining Radiation Hybrid Mapped Transcripts

The UNIGENE database is a repository for transcripts which have been mapped by taking representative Expressed Sequence Tagged Sites (ESTs) and performing PCR analysis on a panel of radiation hybrids which have been calibrated with respect to a framework of 1000 genetic markers (Schuler et al. 1996). We found 36 EST clusters which had been mapped to a radiation hybrid map interval which corresponded to the 18q21 region of interest and to flanking regions outside.

All the ESTs were tested by PCR on our YAC genomic clones to determine which were present. We found approximately half of the ESTs to be present within the genomic clones and were able to order them based on their position within the YAC contig.

Results

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Several clones from our direct selection experiments showed sequence homology to a known EST which we had previously shown to be present in two of the YACs within the contig. The EST was representative of a cluster of sequences. All of these sequences were assembled together using DNAStar Seqman and the consensus sequences obtained were used iteratively to search for other database members within both Unigene, dbEST and EMBL databases. This resulted in the surprising identification of two further clusters of ESTs which had previously not been related to each other on the basis of sequence analysis. The two new EST clusters were annotated as having sequence similarity to ned-4. This was an unexpected finding since we had recently mapped the human ned-4 by Fluorescence In Situ Hybridisation (FISH) to chromosome 15. We were aware that ned-4 was involved in neuronal cell signalling and we concluded that the EST cluster on 18q21 must represent a closely related gene and therefore likely to be involved in affective neurological disorders such as bipolar affective disorder.

The assembly of the EST clusters did not give rise to a single complete contiguous sequence. The reason for this is that many of the EST sequences were derived from IMAGE cDNA clones for which end sequence only was available. In order to fill in the gaps and give a complete contig. four of these clones (IMAGE I.D. 80951, 33059, 79526 and 79984) were sequenced completely to fill the gaps and give an entire complete contiguous sequence. Comparison of the sequence with ned-4 showed that the contig comprised 2kb of 3 Untranslated Region (UTR) and 700bp of the coding region of a gene

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which had approximately 85% identity at the amino acid level to ned-4 and which we named ZGGBP1.

Isolation of the full length gene for ZGGBP1

The extending of partial transcripts to full length clones can be a complex and difficult process requiring skill and expertise for success. Having considered several possibilities, we opted for a PCR-based approach to isolate and characterise the full length ZGGBP1 gene. Human foetal brain double stranded cDNA was synthesised from mRNA using standard methods (Sambrook et al. 1989) and ligated into lambda Zap vector by use of adapters. However, in order to minimise the loss of transcripts often seen following the cloning step, the resulting ligation mix was not cloned but was instead used as a template for PCR. Oligonucleotide primers specific to ZGGBP1 were used in combination with vector specific primers to amplify DNA across the unknown part of the gene. Since the distance to be covered was unknown, we performed long PCR using the commercially available BCL Expand enzyme and long (30mer) oligonucleotide primers. Since we were using unamplified material, where our target cDNAs were likely to be present only in very small amounts, we utilised a secondary PCR step with nested oligonucleotide primers and again using long PCR to yield sufficient PCR products to be visible by gel analysis and also to minimise the possibility of non-specific PCR amplification. The PCR products derived from these experiments were then purified and sequenced directly. Where necessary, the DNA sequence obtained was used to design further primers to walk along the gene in a 3' - 5' direction. The complete nucleotide sequence derived from this work is 5.2kb and the translated amino acid sequence is shown in SEQ ID NO: 1.

The amino acid sequence derived from the cDNA was compared with that of ned-4 and is shown in Figure 2. The proteins diverge markedly towards the N-terminal portion of the protein, although there is conservation of the common functional motifs.

Northern analysis using a probe derived from the 3 UTR of ZGGBP1 showed a band at approximately 4.8kb but also a more abundant band of 9kb in size in several neurological tissues, with the exception of medulla or spinal cord. These bands are likely to be due to alternative splicing (Figure 3). Other tissues contained the 4.8kb band at higher abundance with respect to the 9kb band and also a 4kb band. ZGGBP1 was

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expressed in all tissues examined with the exception of liver where we could not detect a transcript at our current detection sensitivity.

Comparison of Amino Acid Sequences of human ned-4 and ZGGBP1

A comparison of the amino acid sequences of human ned-4 and ZGGBP1 is shown in Figure 6. The two proteins have a high level of homology over much of the C-terminal region, including the Hect and WW domains, but diverge over the central portion of the protein. There is a further block of homology near to the N-terminal region. including the C2 domain. The presence of these domains in ZGGBP1 suggests some common functionality with ned-4.

Identification of polymorphic variants of ZGGBP1

500bp regions of the ZGGBP1 cDNA were PCR amplified from a variety of tissues and lymphoblastoid cell lines. Sequencing was carried out and polymorphisms identified as outlined in Figures 5 and 6. Some intronic sequence had been identified from a genomic clone and sequence analysis of these regions identified a further polymorphic variant as outlined in Figure 7. A tetranucleotide repeat (GATT) was also identified in an intronic sequence derived from this BAC and this was found to have variable numbers of repeats (Figure 8).

Isolation of Genomic Clone for ZGGBP1

The Research Genetics human Bacterial Artificial Chromosome (BAC) library (Shizua et al. 1992, Kim et al. 1996) was screened by PCR using primers specific to the 3'UTR of ZGGBP1 and BACs were isolated. These are being used to characterise the structural gene including the intron/exon structure and the 5' regulatory region.

Isolation of Mouse homologue for ZGGBP1

The full length sequence of ZGGBP1 shown in SEQ ID NO: 1 was used to search the dbEST database to identify homologous mouse sequences. Three overlapping IMAGE clones were identified (IMAGE I.D.479436, 573510, 482922) comprising a partial transcript. Comparison of the mouse and human nucleotide sequence is shown in Figure 4. The mouse clones were isolated for use as a probe for in situ hybridisation on sections

of mouse brain during development, and as a probe of mouse genomic libraries to isolate genomic clones and to produce transgenic mice by gene targeting using homologous recombination.



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- 1. A polynucleotide comprising a nucleic acid sequence which encodes the polypeptide of Seq ID No 2, and homologues and fragments thereof.
- 2. A polynucleotide as claimed in claim 1 which comprises the cDNA sequence of Seq ID No 1.
- 3. Polymorphic variants of the polynucleotide as claimed in claim 2, selected from the group in which:
 - 1) T at position 3554 is replaced by C.
 - ii) C at position 4828 is replaced by G.
 - iii) T within an intronic region associated with ZGGBP1 is replaced by C.
 - iv) C is inserted at position 4032.
 - 4. A polynucleotide which comprises an animal homologue of the nucleic acid claimed in claims 1-3.
- 5. A polynucleotide as claimed in claim 4 which comprises the cDNA sequence of Seq 20 ID No 3, and homologues and fragments thereof.
 - 6. A polynucleotide which is capable of specifically hybridising to eight or more contiguous nucleotides comprised in Seq ID No 1 or Seq ID No 3 or comprised in the complementary strands thereof.
 - 7. A polynucleotide which comprises a ZGGBP1 gene fragment.
 - 8. A vector comprising a polynucleotide of claims 1-7.
- 30 9. A host cell transformed with a vector of claim 8.

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or

or

- 10. A polypeptide comprising the amino acid sequence of Seq ID No 2 and homologues and fragments thereof.
- 11. A polypeptide comprising the amino acid sequence of Seq ID No 4 and homologues and fragments thereof.
 - 12. A fusion protein in which a polypeptide of claim 10 or claim 11 is fused with glutathione-S-transferase.
- 10 13. A method for producing cells which express a polypeptide of claim 10 or claim 11 or a fusion protein of claim 12, comprising:
 - a) culturing a host cell of claim 9 under conditions suitable for the expression of the polypeptide.
 - b) recovering the polypeptide from the host cell culture.
 - 14. A method for identifying a compound capable of modulating the activity of a ZGGBP1 protein , which method comprises subjecting one or more test compounds to a screen comprising:
 - a) a protein as claimed in claims 10-12 or a homologue or fragment thereof,
 - b) a polynucleotide as claimed in claims 1-7 or a homologue or fragment thereof,
 - a host-cell expressing a polypeptide of a ZGGBP1 molecule, and measuring an effect of the test compound on ZGGBP1 activity.
 - 15. A compound that modulates the activity of a human ZGGBP1 identified by the method of claim 14.
- 16. A pharmaceutical composition comprising a compound that modulates the activity of a protein identified by the method of claim 14.

- 17. A diagnostic assay for the detection of ZGGBP1, which assay comprises measuring the presence or absence of a protein as claimed in claims 10-12 or a polynucleotide as claimed in claims 1-7.
- 5 18. An antisense molecule comprising a complement of the polynucleotide in claims 1-7 or a biologically effective fragment thereof.
 - 19. Use of a polynucleotide as claimed in claims 1-7 or claim 18 in gene therapy.
- 10 20. An antibody specific for a protein of claims 10-12 or fragments thereof.
 - 21. A set of amplification primers for selective amplification of a ZGGBP1 gene sequence.

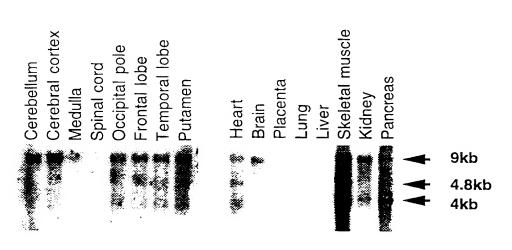


FIGURE 1

MFRLRSWASSTTGSRYGSAFCGSPTLAWCVCVPVCYGESRILRVKVVSG IDLAKKDIFGASDPYVKLSLYVADENRELALVQTKTIKKTLNPKWNEEF YFRVNPSNHRLLFEVFDENRLTRDDFLGOVDVPLSHLPTEDPTMERPYT ^^^^^^ FKDFLLRPRSHKSRVKGFLRLKMAYMPKNGGODEENSDORDDMEHGWEV VDSNDSASQHQEELPPPPLPPGWEEKVDNLGRTYYVNHNNRTTQWHRPS ********* LMDVSSESDNNIRQINQEAAHRRFRSRRHISEDLEPEPSEGGDVPEPWE TISEEVNIAGDSLGVVLPPPPASPGSRTSPQELSEELSRRLQITPDSNG EQFSSLIQREPSSRLRSCSVTDAVAEOGHLPPPSVAYVHTTPGLPSGWE ERKDAKGRTYYVNHNNRTTTWTRPIMQLAEDGASGSATNSNNHLIEPQI RRPRSLSSPTVTLXAPLEGAKDSPVRRAVKDTLSNPQSPQPSPYNSPKP QHKVTQSFLPPGWEMRIAPNGRPFFIDHNTKTTTWEDPRLKFPVHMRSK TSLNPNDLGPLPPGWEERIHLDGRTFYIDHNSKITQWEDPRLQNPAITG ********* PAVPYSREFKQKYDYFRKKLKKPADIPNRFEMKLHRNNIFEESYRRIMS VKRPDVLKARLWIEFESEKGLDYGGVAREWFFLLSKEMFNPYYGLFEYS ATDNYTLOINPNSGLCNEDHLSYFTFIGRVAGLAVFHGKLLDGFFIRPF YKMMLGKQITLNDMESVDSEYYNSLKWILENDPTELDLMFCIDEENFGQ TYQVDLKPNGSEIMVTNENKREYIDLVIQWRFVNRVQKQMNAFLEGFTE LLPIDLIKIFDENELELLMCGLGDVDVNDWROHSIYKNGYCPNHPVIOW FWKAVLLMDAEKRIRLLOFVTGTSRVPMNGFAELYGSNGPOLFTIEOWG SPEKLPRAHTCFNRLDLPPYETFEDLREKLLMAVENAOGFEGVD.



1	SFFSSSSSSTVACPGRGPAPPVCWKRSEMA TCAVEVFCL MERLRSWASSTTGSRYGSAFC-GSPTLAWOVCVPVCYG	P46934 DGGBP-1
3 9 3 8	L F	P46934 2GGBP-1
79 73	M N C V - L T S V Q T K T 1 K K S L N P K W N E E 1 L F R V H P Q Q H P L L F E D E N R E L A L V Q T K T 1 K K T L N P K W N E E F Y F R V N P S N H F L L F E	P46934 2GGBP-1
118 113	V F D E N R L T R D D F L G C V D V P L Y P L P T E N P R L E F P Y T F K D F V V F D E N R L T R D D F L G C V D V F L S H L P T E D P T M E F P Y T F K D F L	F46934 2GGBP-1
158 153	L H F R S H F S R V F G Y L R L F M T Y L P K T S G S E D D N A E Q A F E L E P L R F R S H F S R V F G F L R L F M A Y M P K N G G Q D E E N S D Q R F D M E H	F46934 2GGBP - 1
198 193	G W V V L D C P D A A C H L O O C O E P S P L P P G W E E R O D T L G F T Y Y V G W E V V D S N D S A S O H C E E L P P P P L P P G W E E R V D N L G F T Y Y V	P46934 2GGBP 1
238 233	N H E S F R T C W K P P T P Q D N L T D A E N G N I O L Q A Q R 1 F T T R N H N N R T T Q W H R P S L M D V S S E S D N N I R Q I N C E A A H F F F R S R	P46934 EGGBP-1
275 273	RH 1 S E C L EPEPS PS EG C D V PEPW ET I S E EVN I A G D S L G V V L P	P46934 2GGBP-1
313 313	PESSNULUV - PTHLAEELNARLTIFGNSAVSOPALSSNHPEFASFOSRTSPQELSEELSRRLQITPDSNGEQFSLLIOR	P46934 ZGGBP-1
350 353	S S F · · · P G S L O A Y T F E F Q P T L P · · · · · V L L P T S S G L P P G W E E P S S R L F S C S V T D A V A E Q G H L P P P S V A Y V P T T P G L P S G W E	P46934 EGGBP-1
383 393	E F C DE R G R S Y Y V D H N S R T T T W T K P T V Q A T V E E F F D A K G R T Y Y V N H N N R T T T W T R P I M Q L A E D G A S G C A T N S	P46934 2GGBP-1
414 433	T S O L T S S Q S S - · · · · · · · · · A G P Q S Q A S T S D · · · · · · · · · · · · A G P Q S Q A S T S D · · · · · · · · · · · · · · · · · ·	P46934 ZGGBP-1
435 473	T L SN P Q S P Q P S P Y N S P P P Q H K V T Q S F L P F G W E M R I A P N G P	P46934 ZGGBP-1
464 513	P F F I D H N T K T T T W E D P F L F I P A H L R G K T S I D T S N D L G P L P P F F I D H N T K T T T W E D P F L F P V H M R S K T S L N + P N D L G P L P	P46934 ZGGBP-1
504 552	P G W E E R T H T D G R I F Y I N H N I K R T Q W E D P R L E N V A I T G P A V F G W E E R I H L D G R T F Y I D H N S K I T Q W E D P R L Q N P A I T G P A V	P46934 ZGGBP-1
544 592	PYSRDYKRKYEFFRRKLKKONDIPNKFEMELRRATVLEDS PYSREFKOKYDYFRKKLKKPADIPNRFEMELKRNNIFEES	P46934 ZGGBP-1
584 632	Y R R I M G V K R A D F L K A R L W I E F D G E K G L D Y G G V A R E W F F L L Y F R I M S V K R P D V L K A R L W I E P E S E K G L D Y C G V A R E W F F L L	P46934 ZGGBP-1
62 4 672	S F E M F N P Y Y G L F E Y S A T D N Y T L Q I N P N S G L C N E D H L S Y F K S F E M F N P Y Y G L F E Y S A T D N Y T L Q I N P N S G L C N E D H L S Y F T	P46934 ZGGBP-1
66 4 712	FIGRVAGMAVYHGKLLDGFFIRPFYKMMLHKPITLHDMES FIGRVAGLAVFHGKLLDGFFIRPFYKMMLGKCITLNDMES	P46934 2GGBP-1
704 752	V D S E Y Y N S L R W I L E N D P T E L D L R F ! I D E E L F G Q T H Q H E L K V D S E Y Y N S L K W I L E N D P T E L D L M F C ! D E E N F G Q T Y Q V D L K	P46934 2GGBP-1
744 792	N G G S E I V V T N K N K K E Y I Y L V I Q W R F V N R I Ç K Ç M A A F K E G F P N G S E I M V T N E N K R E Y I D L V I O W R F V N R V Q K Q M N A F L E G F	P46934 ZGGBP-1
784 832		P46934 ZGGBP-1
824 872		P46934 ZGGBP-1
864 912		P46934 IGGBP 1
914 952	ENFELLMENTOPFOGV ETFELLREVILMANENAOGFEGVO	P46934 DGGBF-1





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25 STTCTTCTTACTGTCCAAAGAGATGTTTAACCCCCTACTAT Mouse 230	
65 GGCCTCTTCGAGTACTCTGCCACGGACAACTACACACATCC Mouse 23:	
105 A G A T C A A T C C C A A C T C A G G C C T C T G T A A T G A A G A C C A T T T Mouse 230 121 A G A T C A A C C C T A A T T C A G G C C T C T G T A A T G A G G A T C A T T T Human 230	SBF 1
145 GTCCTATTTCACCTTCATTGGAAGAGTTGCTGGCCTAGCG Mouse 2361 GTCCTACTTTATTGGAAGAGTTGCTGGTCTGGCC Human 23	GBF - 1
185 3 T G T T T C A T G G G A A A C T C T T A G A T G G A T T C T T C A T T C G A C Mouse 23-201 5 T A T T T C A T G G G A A G C T C T T A G A T G G T T T C T T C A T T A G A C Human 23-3	
225 CATTCTACAAGATGATGCTGGGGAAGCAGATAACGCTGAA Mouse 2G. 241 CATTTTACAAGATGATGTTGGGGAAAGCAGATAACCCTGAA Human 23	
265 C G A C A T G G A G T C C G T G G A C A G C G A G T A C T A C A A C T C T T T G Mouse 230 281 T G A C A T G G A A T C T G T G G A T A G T G A A T T A C A A C T C T T T G Human 230	3BF - 1
305 A A G T G G A T C T T A G A A A C G A C C C C A C G G A A C T T G A C C T C A Mouse 2330 321 A A A T G G A T C C T G G A G A A T G A C C C T A C T G A G C T G G A C C T C A Human 2330	GBF1
345 T G T T C T G C A T A G A C G A W G A G A A C T T T G G G C A G A C A T A C C A Mouse 2330 361 T G T T C T G C A T A G A C G A A G A A A C T T T G G A C A G A C A T A T C A Human 2350	GBP-1
385 A G T G G A T C T G A A G C C C A A C G G G T C A G A A A T A A T G G T A A C C Mouse 2000 401 A G T G G A T T T G A A G C C C A A T G G G T C A G A A A T A A T G G T C A C A Human 203	
425 A A T G A G A A C G A G A A T A C A T T G A C T T A G T C A T C C A G T Mouse 236 441 A A T G A A A A A A A A A G G G A A T A T	
465 G G A G A T T T G T G A A C A G G G T C C A G A A G C A A A T G A A T G C C T T Mouse 23.	
505 TTTGGAGGGATTTACAGAACTTCTTCCAATTCGACTTGATT Mouse CGC 521 TTTGGAGGGATTCACAGAACTACTTCCTATTGATTTGAT	
545 A A A A T T T T T G A T G A A A A T G A G C T G G A G T T G C T G A T G T G C G House 256 A A A A T T T T T G A T G A A A A T G A G C T G G A G T T G C T C A T G T G C G Human 256	
585 GCCTTGGTGATGTCGACGTGAACGACTGGAGACAGCACTC Mouse 230 601 GCCTCGGTGATGTGGATGTGAATGACTGGAGACAGCATTC Human 230	
625 TATTTACAAGAACGGCTACTGCCCCAACCACCCTGTCATC Mouse 2396	
665 TAGTGGTTCTGGAAGGCCGTGCTGCTGATGGATGCTGAGA Mouse ZGG	
705 A G C G C A T C C G G T T A C T A C A G T T T G T C A C A G G C A C C T C C A G Mouse ZGC 721 A G C G T A T C C G G T T A C T G C A G T T T G T C A C A G G G A C A T C G C G Human 2Gc	
745 AGTACCCATGAATGGATTTGCCGAACTCFATGGTTCCAAT Mouse 239	
785 GGTCCTCAGCTGTTTACAATAGAGCAATGGGGCAGTCC]- G Mouse 2G 801 GGTCCTCAGCTGTTTACAATAGAGCAATGGGGCAGTCCTG Human 23	
824 AAAACTACC-AGAGCTU TACATGCTT AATCGC Mouse 3G 841 AGAAACTGCCCAGAGCTCACACGCTTTAATCGCCTTG Human, 2G	





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602 961	AACTTCCTCCTCCTCTCTGCCTCCCGGGTGGGAAGAAA Pub-3.seq
642	AGTGGACAATTTAGGCCGAACTTACTATGTCAACCAAAC Pub-3.seq AGTGGACAATTTAGGCCGAACTTACTATGTCAACCACAA ZGGBP1.seq
682 1041	AACCGGACCACTCAGTGGCACAGACCAAGCCTGATGGACG Pub-3.seq AACCGGACCACTCAGTGGCACAAAGCCTGATGGACG ZGGBP1.seq
722 1081	TGTCCTCGGAGTCGGACAATAACATCAGACAGATCAACCA TGTCCTCGGAGACAATAACATCAGACAGATCAACCA
762 1121	GGAGGCAGCACCGGCGCTTCCGCTCCCGCAGGCACATC Pub-3.seq GGAGGCAGCACACGGCGTTCCGCTCCCGCAGGCACATC ZGGBP1.seq
802	AGCGAAGACTTGGAGCCCGAGCCCTCGGAGGGGGGGATG Pub-3.seq AGCGAAGACTTGGAGCCCGAGCCCTCGGAGGGGGGGGATG ZGGBP1.seq
842 1201	TCCCCGAGCCTTGGGAGACCATTTCAGAGGAAGTGAATAT Pub-3.seq TCCCCGAGCCTTGGGAGACCATTTCAGAGGAAGTGAATAT ZGGBP1.seq
882 [0]	CGCTGGAGACTCTCGGTCTGGCTCTGCCCCCACCACCG Pub-3.seq CGCTGGAGACTCTCGGTGTGTTTTGCCCCCACCACCG ZGGBP1.seq
922 [6 1281 [6	GTCTCCCCAGGATCTCGGACCAGCCCTCAGGAGCTGTCAG Pub-3.seq GCCTCCCCAGGATCTCGGACCAGCCCTCAGGAGCTGTCAG ZGGBP1.seq
962 7	AGGAACTAAGCAGAAGGCTTCAGATCACTCCAGACTCCAA Pub-3.seq AGGAACTAAGCAGAAGGCTTCAGATCACTCCAGACTCCAA ZGGBP1.seq
1002	TGGGGAACAGTTCAGCTCTTTGATTCAAGAAACCCTCC Pub-3.seq TGGGGAACAGTTCAGCTCTTTGATTCAAAGAGAACCCTCC 2GGBP1.seq
1042 T	TCAAGGTTGAGGTCATGCAGTGTCACCGACGCAGTTGCAG Pub-3.seq TCAAGGTTGAGGTCATGCAGTGTCACCGACGCAGTTGCAG ZGGBP1.seq
1082 A	AACAGGGCCATCTACCACCGCCATCAGTGGCCTATGTACA Pub-3.seq AACAGGGCCATCTACCACCGCCATCAGTGGCCTATGTACA ZGGBP1.seq



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1562 GTTTGAAATTTCCAGTACATATGCGGTCAAAGACATCTTT Pub-3.seq 1921 GTTTGAAATTTCCAGTACATATGCGGTCAAAGACATCTTT ZGGBP1.seq
1602 A A A C C C C A A T G A C C T T G G C C C C T T C C T G G C T G G G A A Pub-3.seq 1961 A A A C C C C A A T G A C C T T G G C C C C T T C C T G G C T G G G A A ZGGBP1.seq
1642 GAAAGAATTCACTTGGATGGCCGAACGTTTTATATTGATC Pub-3.seq 2001 GAAAGAATTCACTTGGATGGCCGAACGTTTTATATTGATC ZGGBP1.seq
1682 ATAATAGCAAAATTACTCAGTGGGAAGACCCAAGACTGCA Pub-3.seq 2041 ATAATAGCAAAATTACTCAGTGGGAAGACCCAAGACTGCA ZGGBP1.seq
1722 GAACCCAGCTATTACTGGTCCGGCTGTCCCTTACTCCAGA Pub-3.seq 2081 GAACCCAGCTATTACTGGTCCGGCTGTCCCTTACTCCAGA ZGGBP1.seq
1762 GAATTTAAGCAGAAATATGACTTCAGGAAGAATTAA Pub-3.seg 2121 GAATTTAAGCAGAAATATGACTACTTCAGGAAGAATTAA 2GGBP1.seg
1802 AGAAACCTGCTGATATCCCCAATAGGTTTGAAATGAAACT Pub-3.seq 2161 AGAAACCTGGTATATCCCCAATAGGTTTGAAATGAAACT ZGGRP1.seq
1842 TCACAGAAATAACATATTTGAAGAGTCCTATCGGAGAATT Pub-3.seq 2201 TCACAGAAATAACATATTTGAAGAGTCCTATCGGAGAATT ZGGBP1.seq
1882 ATGTCCGTGAAAAGACCAGATGTCCTAAAAGCTAGACTGT Pub-3.seq 2241 ATGTCCGTGAAAAGACCAGATGTCCTAAAAGCTAGACTGT ZGGBP1.seq
1922 GGATTGAGTTTGAATCAGAGAAAGGTCTTGACTATGGGG G Pub-3.seq 2281 GGATTGAGTTTGAATCAGAGAAAGGTCTTGACTATGGGGG ZGGBP1.seq
1962 TGTGGCCAGAGAATGGTTCTTTACTGTCCAAAGAGATG Pub-3.seq 2321 TGTGGCCAGAGAATGGTTCTTACTGTCCAAAGAGATG ZGGBP1.seq
2002 TTCAACCCCTACTACGGCCTCTTTGAGTACTCTGCCACGG Pub-3.seq 2361 TTCAACCCCTACTACGGCCTCTTTGAGTACTCTGCCACGG ZGGBP1.seq
2042 A C A A C T A C A C C C T T C A G A T C A A C C C T A A T T C A G C C T C T G Pub-3.seq 2401 A C A A C T A C A C C C T T C A G A T C A A C C C T A A T T C A G G C C T C T G ZGGBP1.seq

2082 TAATGAGGATCATTTGTCCTACTTCACTTTTATTGGAAGA Pub-3.seg
2202 G C A G A T A A C C C T G A A T G A C A T G G A A T C T G T G G A T A G T G A A Pub-3. seq 2561 G C A G A T A A C C C T G A A T G A C A T G G A A T C T G T G G A T A G T G A A ZGGBP1. seq
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2442 GCAGATGAACGCCTTCTTGGAGGGATTCACAGAACTACTT Pub-3.seq 2801 GCAGATGAACGCCTTCTTGGAGGGATTCACAGAACTACTT ZGGBD1.seq
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2522 AGTTGCTCATGTGCGGCCTCGGTGATGTGGATGTGAATGA Pub-3.seq 2881 AGTTGCTCATGTGCGGCCTCGGTGATGTGGATGTGAATGA ZGGBP1.seq
2562 CTGGAGACAGCATTCTATTTACAAGAACGGCTACTGCCCA Pub-3.seq 2921 CTGGAGACAGCATTCTATTACAAGAACGGCTACTGCCCA ZGGBP1.seq
2602 A A C C A C C C G T C A T T C A G T G G T T C T G G A A G G C T G T A C Pub-3.seq 2961 A A C C A C C C C G T C A T T C A G T G G T T C T G G A A G G C T G T G C T A C ZGGBP1.seq
2642 TCATGGACGCCGAAAAGCGTATCCGGTTACTGCAGTTTGT Pub-3.seq 3001 TCATGGACGCCGAAAAGCGTATCCGGTTACTGCAGTTTGT ZGGBP1.seq
2682 CACAGGGACATCGCGAGTACCTATGAATGGATTTGCCGAA Pub-3.seq 3041 CACAGGGACATCGCGAGTACCTATGAATGGATTTGCCGAA ZGGBP1.seq
2722 CTTTATGGTTCCAATGGTCCTCAGCTGTTTACAATAGAGC Pub-3.seq 3081 CTTTATGGTTCCAATGGTCCTCAGCTGTTTACAATAGAGC ZGGBP1.seq
2762 A A T G G G C A G T C C T G A G A A C T C C C A G A G C T C A C A C A T G Pub-3.seq 3121 A A T G G G C A G T C C T G A G A A C T G C C C A G A G C T C A C A T G ZGGBP1.seq
2802 CTTTAATCGCCTTGACTTACCTCCATATGAAACCTTTGAA Pub-3.seq 3161 CTTTAATCGCCTTGACTTACCTCCATATGAAACCTTTGAA ZGGBP1.seq
2842 GATTTACGAGAGAAACTTCTCATGGCCGTGGAAAATGCTC Pub-3.seq 3201 GATTTACGAGAAACTTCTCATGGCCGTGGAAATGCTC ZGGBP1.seq
2882 AAGGATTTGAAGGGGTGGATTAAGCACCCTGTGCCTCGGG Pub-3.seq 3241 AAGGATTTGAAGGGGTGGATTAAGCACCCTGTGCCTCGGG ZGGBP1.seq
2922 GGTGGTTGTTCTTCAAGCAAGTTCTGCTTGCACTTTTGCA Pub-3.seq 3281 GGTGGTTGTTCTTCAAGCTAGTTCTGCTTGCACTTTGCA ZGGBP1.seq
2962 TTTGCCTAACAGACTTTTGCAGAGGCGATGGCAGAGAGCA Pub-3.seq 3321 TTTGCCTAACAGACTTTTGCAGAGGCGATGGCAGAGAGCA ZGGBP1.seq
3002 GCTGCAGGCATGGTCCCTGGAGCCGAGCCTTCACCACGCA Pub-3.seq 3361 GCTGCAGGCATGGTCCCTGGAGCCGAGCCTTCACCACGCA ZGGBP1.seq

AGTACTTTGAGAGAATTTCCAATATATAGAC ZGGP1.seq	GATAATTTTTCCATACTCAGAATGAAAACTGGA] ZGGBP1.seq		AGCTACAGGCTGAGAATTGTAACATAGCATGAC	rrgrgtrgactrgaaaggaatcacacattatrcc zggBP1.seq	AGTAATTACATGTGTTCTAACACATTTGAGACAGG ZGGBP1.seq	NCTCCCATTTCTCATCCGAGAAATTACTTAACCT] 25GBP1.seq	3GCGCTGTACAGTCATTTATTCTATTTCTT ZGGBF1.seq	STTTGTAGTAGAGACATTTTGAATGAAACTTGGCA 233RP1.seq	GATTCAAAACTGTGGAAACCAGATCTGTTTAGTC ZGGBP1.seq	TTGTATGCGTTTGCTAATGGTAGCTAAATAACCA) 233BP1.seq	GTTGTAAATGCACCAATTCTGAAGGCACTTTATG ZGGBP1.seq	Pub-3.seq
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TCCGGTGCAATATCTATCAATTGTGAATCT GTATAAAAACCTGGATGTAAAGCTGAGCCT CCTCACCAACTGTTTGTGATTCTACTCA TTTATTTAATGTACTCTTAATCTAACTGAG AATGACCTGTTGCATTAATCTGAGTGT		AGTTGTGCCTCTTGTGTGCTAGATTAAAAGT
TCCGGTGCAATATCTATCAATTGTGAATCT GTATAAAAACCTGGATGTAAAGCTGAGCCT CCTCACCAACTGTTTTGTGATTTCTACTCA TTTATTTAATGTACTCTTAATCTAACTGAG		CCAATGACCTGTTGCATGCTTCAATACCGTG
TCCGGTGCAATATCTATCAATTGTGAATCT GTATAAAAACCTGGATGTAAAGCTGAGCCT CCTCACCAACTGTTTGTGAATCTACTCA		TTTATTTAATGTACTCTTAATCTGA
TCCGGTGCAATATCTATCAATTGTGAATCT		CCTCACCAACTGTTTTGTGATTTCTACTC
TCCGGTGCAATATCTATCAATTGTGAATCT		GTATAAAACCTGGATGTAAAGCTGAGCC
	_	TCCGGTGCAATATCTATCAATTGTGAATC

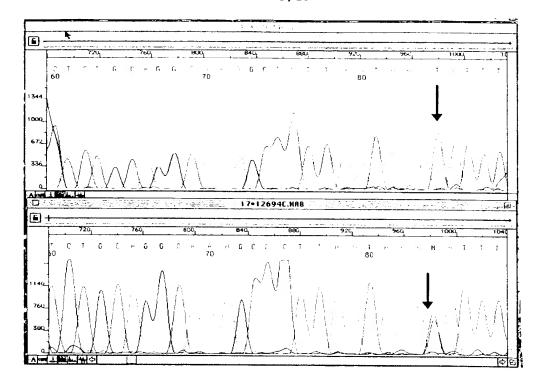
FIGURE 5 continued

3214	Pub-3.seq ZGGBP1.seq
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3214	Pub-3.seq ZGGBP1.seq
3220	Pub-3.seq ZGGBP1.seq
3220	Pub-3.seq ZGGBP1.seq
3220	Pub-3.seq ZGGBP1.seq
3220 AAAAAA	Pub-3.seq ZGGBP1.seq
3226 5080 A G C T G A G T T G G T T C C T T T T T C C T T A T T G G T T G A A A T T A ZC	Pub-3.seg ZGGBP1.seq
3226 5120 CCT GGT A GT GAT CAGAAAACTTAGATGCTATRTAACT C	Pub-3.seq ZGGBP1.seq

Decoration 'Decoration #1': Box residues that match the Consensus exactly.



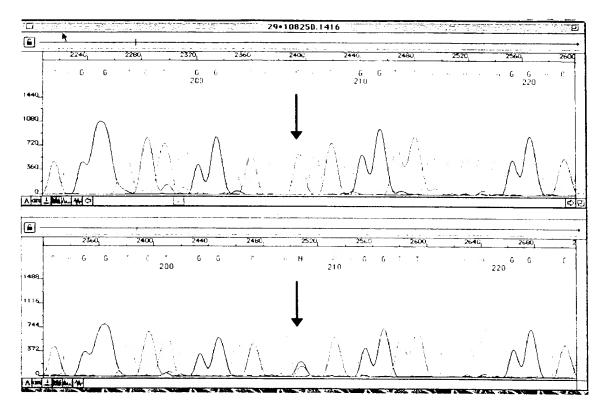




Wild Type (human foetal brain) Variant Type (human adult brain) Polymorphism Position	T/T T/C 3554		
		RFLP	-

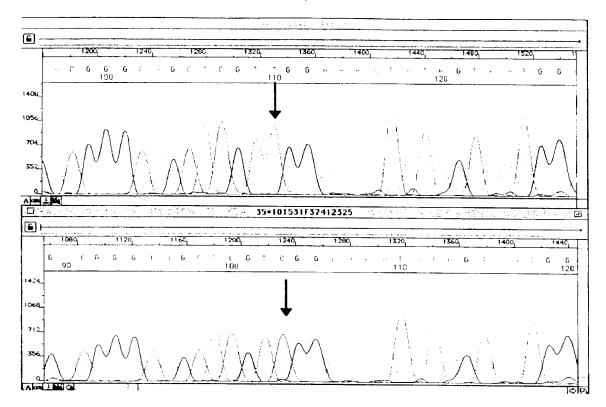


16/19



Wild Type (GM1416) C/C Variant (7225) C/G Position 4828

17/19



Primer sequences derived from BAC and used on lymphoblastoid cell lines from BPAD Patients.

Homozygous wild type (KK169) - T/T

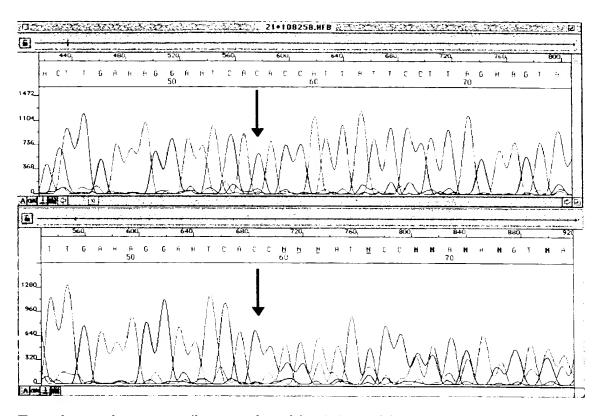
Homozygous variant (KK232) - C/C



Figure 9

Tetranucleotide repeat underlined





Top electropherogram (human foetal brain) - wild type

Lower electropherogram (7225)

- heterozygous variant

Arrow indicates the position of the C+C insertion - position 4032

FIGURE 10



-1-

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
 - (A) NAME: Zeneca Limited
 - (B) STREET: 15 Stanhope Gate
 - (C) CITY: London
 - (D) STATE: England
 - (E) COUNTRY: United Kingdom
 - (F) POSTAL CODE (ZIP): W1Y 6LN
 - (G) TELEPHONE: 0171 304 5000
 - (H) TELEFAX: 0171 304 5151
 - (I) TELEX: 0171 304 2042
- (ii) TITLE OF INVENTION: NOVEL COMPOUNDS
- (iii) NUMBER OF SEQUENCES: 5
- (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: Patentln Release #1.0, Version #1.30 (EPO)
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: GB 9716162.4
 - (B) FILING DATE: 01-AUG-1997
- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5154 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CAAGCGCGCA ATTAACCCTC ACTAAAGGGA ACACCAACAC GTCGCCAGGA CTGCGCCGTT 60

CGCTGCGCTC ATAGGCGGCG ATTTCATCAA GGGTGGCAAG GATCGCCTGG TCGACGGTCA $120\,$

GGTCGTCCTC GACGCGGTTG CCCTCCTCGT CCTGTTCCAG GGTGAGTGGG CGATACCAGG 180

TGTCCACCGG GAAGGTACGG CCCGACACCT CGACAATCGG CGCATCGTCG AAGTGCTTGG 240

AAAAGCGCTC CAGGTCGATG GTGGCCGAGG TGATGATGAC TTTCAGGTCG GGGCGACGCG 300

GCAACAGGGT CTTGAGGTAG CCGAGCAGGA AGTCGATGTT CAGGCTGCGT TCGTGGGCTT 360

CGTCGACGAC AGGCTCGCGT TATGGCTCCG CTTTCTGCGG CTCTCCTACC CTGGCATGGT 420

GTGTGTGT GCCTGTGTGC TACGGAGAGT CCCGTATTCT CAGAGTAAAA GTTGTTCTGG 480

AATGATCTCG CCAAAAAGGA CATCTTTGGA GCCAGTGATC CGTATGTGAA ACTTTCATTG 540

TACGTAGCGG ATGAGAATAG AGAACTTGCT TTGGTCCAGA CAAAAACAAT TAAAAAGACA 600

CTGAACCCAA AATGGAATGA AGAATTTTAT TTCAGGGTAA ACCCATCTAA TCACAGACTC 660

CTATTTGAAG TATTTGACGA AAATAGACTG ACACGAGACG ACTTCCTGGG CCAGGTGGAC 720

GTGCCCCTTA GTCACCTTCC GACAGAAGAT CCAACCATGG AGCGACCCTA TACATTTAAG 780

GACTTTCTCC TCAGACCAAG AAGTCATAAG TCTCGAGTTA AGGGATTTTT GCGATTGAAA 840

ATGGCCTATA TGCCAAAAAA TGGAGGTCAA GATGAAGAAA ACAGTGACCA GAGGGATGAC 900

ATGGAGCATG GATGGGAAGT TGTTGACTCA AATGACTCGG CTTCTCAGCA CCAAGAGGAA 960

CTTCCTCCTC CTCCTCTGCC TCCCGGGTGG GAAGAAAAG TGGACAATTT AGGCCGAACT 1020

TACTATGTCA ACCACAACAA CCGGACCACT CAGTGGCACA GACCAAGCCT GATGGACGTG 1080

TCCTCGGAGT CGGACAATAA CATCAGACAG ATCAACCAGG AGGCAGCACA CCGGCGCTTC 1140

CGCTCCCGCA GGCACATCAG CGAAGACTTG GAGCCCGAGC CCTCGGAGGG CGGGGGATGTC 1200

CCCGAGCCTT GGGAGACCAT TTCAGAGGAA GTGAATATCG CTGGAGACTC TCTCGGTGTG 1260

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CAGGGCCATC TACCACCGCC ATCAGTGGCC TATGTACATA CCACGCCGGG TCTGCCTTCA 1500

GGCTGGGAAG AAAGAAAGA TGCTAAGGGG CGCACATACT ATGTCAATCA TAACAATCGA 1560

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ACAAACAGTA ACAACCATCT AATCGAGCCT CAGATCCGCC GGCCTCGTAG CCTCAGCTCG 1680

CCAACAGTAA CTTTATTGCC CCGCTGGAGG GTGCCAAGGA CTCACCCGTA CGTCGGGCTG 1740

TGAAAGACAC CCTTTCCAAC CCACAGTCCC CACAGCCATC ACCTTACAAC TCCCCCAAAC 1800

CACAACACA AGTCACACAG AGCTTCTTGC CACCCGGCTG GGAAATGAGG ATAGCGCCAA 1860

ACGGCCGGCC CTTCTTCATT GATCATAACA CAAAGACTAC AACCTGGGAA GATCCACGTT 1920

TGAAATTTCC AGTACATATG CGGTCAAAGA CATCTTTAAA CCCCAATGAC CTTGGCCCC 1980

TTCCTCCTGG CTGGGAAGAA AGAATTCACT TGGATGGCCG AACGTTTTAT ATTGATCATA 2040

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CTGTCCCTTA CTCCAGAGAA TTTAAGCAGA AATATGACTA CTTCAGGAAG AAATTAAAGA 2160

AACCTGCTGA TATCCCCAAT AGGTTTGAAA TGAAACTTCA CAGAAATAAC ATATTTGAAG 2220

AGTCCTATCG GAGAATTATG TCCGTGAAAA GACCAGATGT CCTAAAAGCT AGACTGTGGA 2280

TTGAGTTTGA ATCAGAGAAA GGTCTTGACT ATGGGGGTGT GGCCAGAGAA TGGTTCTTCT 2340

TACTGTCCAA AGAGATGTTC AACCCCTACT ACGGCCTCTT TGAGTACTCT GCCACGGACA 2400

ACTACACCCT TCAGATCAAC CCTAATTCAG GCCTCTGTAA TGAGGATCAT TTGTCCTACT 2460

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GATTCACAGA ACTACTTCCT ATTGATTTGA TTAAAATTTT TGATGAAAAT GAGCTGGAGT 2880

TGCTCATGTG CGGCCTCGGT GATGTGGATG TGAATGACTG GAGACAGCAT TCTATTTACA 2940

AGAACGGCTA CTGCCCAAAC CACCCCGTCA TTCAGTGGTT CTGGAAGGCT GTGCTACTCA 3000

TGGACGCCGA AAAGCGTATC CGGTTACTGC AGTTTGTCAC AGGGACATCG CGAGTACCTA 3060

TGAATGGATT TGCCGAACTT TATGGTTCCA ATGGTCCTCA GCTGTTTACA ATAGAGCAAT 3120

GGGGCAGTCC TGAGAAACTG CCCAGAGCTC ACACATGCTT TAATCGCCTT GACTTACCTC 3180

CATATGAAAC CTTTGAAGAT TTACGAGAGA AACTTCTCAT GGCCGTGGAA AATGCTCAAG 3240

GATTTGAAGG GGTGGATTAA GCACCCTGTG CCTCGGGGGT GGTTGTTCTT CAAGCAAGTT 3300

CTGCTTGCAC TTTTGCATTT GCCTAACAGA CTTTTGCAGA GGCGATGGCA GAGAGCAGCT 3360

GCAGGCATGG TCCCTGGAGC CGAGCCTTCA CCACGCACTC GTCCAAGTTC GGGATGCGGG 3420

AACCTGGTCC CAGCTTGAGT TCCTGCCTTT CCCACCACAA ATTATCAACT GGTTGATGTG 3480

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TTCGTTATGA TTAAAGATGT CTCATGTACT TGGAAAAGTG AGCATTTTTT
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ACCTCCACCC TCTACTTTAT TAGAATTGGA AGGCAAATTT TTGTCCAAAA ACCTACAGAC 3840

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GACTCCCATT TCTCATCCGA GAAATTACTT AACCCTTCCT GGGCGCTGTA CAGTCATCTT 4140

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TGGCATGTGA GAAGCCATGG AAGGTTGTGG TTGTAAATGA GTTGTCTAAA GGGGTGCAGA 5040

GGCCTGAGGT TTCTAAAAGA AGGTAGATTT CTACAGAGCT GAGTGTTGGT TCCTTTTTCT 5100

TATTGGTTGA AAATTACCTG GTAGTGATCA GAAAACTTAG ATGCTATGTA ACTC 5154

- (2) INFORMATION FOR SEQ ID NO: 2:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 975 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Phe Arg Leu Arg Ser Trp Ala Ser Ser Thr Thr Gly Ser Arg Tyr

1 5 10 15

Gly Ser Ala Phe Cys Gly Ser Pro Thr Leu Ala Trp Cys Val Cys Val 20 25 30

Pro Val Cys Tyr Gly Glu Ser Arg Ile Leu Arg Val Lys Val Val Ser 35 40 45

Gly Ile Asp Leu Ala Lys Lys Asp Ile Phe Gly Ala Ser Asp Pro Tyr 50 55 60

Val Lys Leu Ser Leu Tyr Val Ala Asp Glu Asn Arg Glu Leu Ala Leu 65 70 75 80

Val Gln Thr Lys Thr He Lys Lys Thr Leu Asn Pro Lys Trp Asn Glu 85 90 95

- Glu Phe Tyr Phe Arg Val Asn Pro Ser Asn His Arg Leu Leu Phe Glu 100 105 110
- Val Phe Asp Glu Asn Arg Leu Thr Arg Asp Asp Phe Leu Gly Gln Val 115 120 125
- Asp Val Pro Leu Ser His Leu Pro Thr Glu Asp Pro Thr Met Glu Arg 130 135 140
- Pro Tyr Thr Phe Lys Asp Phe Leu Leu Arg Pro Arg Ser His Lys Ser 145 150 155 160
- Arg Val Lys Gly Phe Leu Arg Leu Lys Met Ala Tyr Met Pro Lys Asn 165 170 175
- Gly Gly Gln Asp Glu Glu Asn Ser Asp Gln Arg Asp Asp Met Glu His 180 185 190
- Gly Trp Glu Val Val Asp Ser Asn Asp Ser Ala Ser Gln His Gln Glu 195 200 205
- Glu Leu Pro Pro Pro Pro Leu Pro Pro Gly Trp Glu Glu Lys Val Asp 210 215 220
- Asn Leu Gly Arg Thr Tyr Tyr Val Asn His Asn Asn Arg Thr Thr Gln 225 230 235 240
- Trp His Arg Pro Ser Leu Met Asp Val Ser Ser Glu Ser Asp Asn Asn 245 250 255
- Ile Arg Gln Ile Asn Gln Glu Ala Ala His Arg Arg Phe Arg Ser Arg 260 265 270
- Arg His Ile Ser Glu Asp Leu Glu Pro Glu Pro Ser Glu Gly Gly Asp 275 280 285
- Val Pro Glu Pro Trp Glu Thr Ile Ser Glu Glu Val Asn Ile Ala Gly 290 295 300
- Asp Ser Leu Gly Val Val Leu Pro Pro Pro Pro Ala Ser Pro Gly Ser 305 310 315 320
- Arg Thr Ser Pro Gln Glu Leu Ser Glu Glu Leu Ser Arg Arg Leu Gln 325 330 335
- Ile Thr Pro Asp Ser Asn Gly Glu Gln Phe Ser Ser Leu Ile Gln Arg 340 345 350

- Glu Pro Ser Ser Arg Leu Arg Ser Cys Ser Val Thr Asp Ala Val Ala 355 360 365
- Glu Gln Gly His Leu Pro Pro Pro Ser Val Ala Tyr Val His Thr Thr 370 375 380
- Pro Gly Leu Pro Ser Gly Trp Glu Glu Arg Lys Asp Ala Lys Gly Arg 385 390 395 400
- Thr Tyr Tyr Val Asn His Asn Asn Arg Thr Thr Thr Trp Thr Arg Pro 405 410 415
- lle Met Gln Leu Ala Glu Asp Gly Ala Ser Gly Ser Ala Thr Asn Ser 420 425 430
- Asn Asn His Leu Ile Glu Pro Gln Ile Arg Arg Pro Arg Ser Leu Ser 435 440 445
- Ser Pro Thr Val Thr Leu Xaa Ala Pro Leu Glu Gly Ala Lys Asp Ser 450 455 460
- Pro Val Arg Arg Ala Val Lys Asp Thr Leu Ser Asn Pro Gln Ser Pro 465 470 475 480
- Gln Pro Ser Pro Tyr Asn Ser Pro Lys Pro Gln His Lys Val Thr Gln 485 490 495
- Ser Phe Leu Pro Pro Gly Trp Glu Met Arg Ile Ala Pro Asn Gly Arg 500 505 510
- Pro Phe Phe Ile Asp His Asn Thr Lys Thr Thr Trp Glu Asp Pro 515 520 525
- Arg Leu Lys Phe Pro Val His Met Arg Ser Lys Thr Ser Leu Asn Pro 530 535 540
- Asn Asp Leu Gly Pro Leu Pro Pro Gly Trp Glu Glu Arg Ile His Leu 545 550 555 560
- Asp Gly Arg Thr Phe Tyr Ile Asp His Asn Ser Lys Ile Thr Gln Trp 565 570 575
- Glu Asp Pro Arg Leu Gln Asn Pro Ala Ile Thr Gly Pro Ala Val Pro 580 585 590
- Tyr Ser Arg Glu Phe Lys Gln Lys Tyr Asp Tyr Phe Arg Lys Lys Leu 595 600 605

- Lys Lys Pro Ala Asp Ile Pro Asn Arg Phe Glu Met Lys Leu His Arg 610 615 620
- Asn Asn Ile Phe Glu Glu Ser Tyr Arg Arg Ile Met Ser Val Lys Arg 625 630 635 640
- Pro Asp Val Leu Lys Ala Arg Leu Trp Ile Glu Phe Glu Ser Glu Lys 645 650 655
- Gly Leu Asp Tyr Gly Gly Val Ala Arg Glu Trp Phe Phe Leu Leu Ser 660 665 670
- Lys Glu Met Phe Asn Pro Tyr Tyr Gly Leu Phe Glu Tyr Ser Ala Thr 675 680 685
- Asp Asn Tyr Thr Leu Gln Ile Asn Pro Asn Ser Gly Leu Cys Asn Glu 690 695 700
- Asp His Leu Ser Tyr Phe Thr Phe Ile Gly Arg Val Ala Gly Leu Ala 705 710 715 720
- Val Phe His Gly Lys Leu Leu Asp Gly Phe Phe Ile Arg Pro Phe Tyr 725 730 735
- Lys Met Met Leu Gly Lys Gln Ile Thr Leu Asn Asp Met Glu Ser Val 740 745 750
- Asp Ser Glu Tyr Tyr Asn Ser Leu Lys Trp Ile Leu Glu Asn Asp Pro 755 760 765
- Thr Glu Leu Asp Leu Met Phe Cys Ile Asp Glu Glu Asn Phe Gly Gln 770 775 780
- Thr Tyr Gln Val Asp Leu Lys Pro Asn Gly Ser Glu Ile Met Val Thr 785 790 795 800
- Asn Glu Asn Lys Arg Glu Tyr Ile Asp Leu Val Ile Gln Trp Arg Phe 805 810 815
- Val Asn Arg Val Gln Lys Gln Met Asn Ala Phe Leu Glu Gly Phe Thr 820 825 830
- Glu Leu Leu Pro Ile Asp Leu Ile Lys Ile Phe Asp Glu Asn Glu Leu 835 840 845
- Glu Leu Leu Met Cys Gly Leu Gly Asp Val Asp Val Asp Asp Trp Arg 850 855 860

Gln His Ser Ile Tyr Lys Asn Gly Tyr Cys Pro Asn His Pro Val Ile 865 870 875 880

- Gln Trp Phe Trp Lys Ala Val Leu Leu Met Asp Ala Glu Lys Arg Ile 885 890 895
- Arg Leu Clin Phe Val Thr Gly Thr Ser Arg Val Pro Met Asn Gly 900 905 910
- Phe Ala Glu Leu Tyr Gly Scr Asn Gly Pro Gln Leu Phe Thr Ile Glu 915 920 925
- Gln Trp Gly Ser Pro Glu Lys Leu Pro Arg Ala His Thr Cys Phe Asn 930 935 940
- Arg Leu Asp Leu Pro Pro Tyr Glu Thr Phe Glu Asp Leu Arg Glu Lys 945 950 955 960
- Leu Leu Met Ala Val Glu Asn Ala Gln Gly Phe Glu Gly Val Asp 965 970 975

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 854 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ACAATGGGG CGTGGCAGAG AATGGTTCTT CTTACTGTCC AAAGAGATGT TTAACCCCTA 60

CTATGGCCTC TTCGAGTACT CTGCCACGGA CAACTACACA CTTCAGATCA ATCCCAACTC 120

AGGCCTCTGT AATGAAGACC ATTTGTCCTA TTTCACCTTC ATTGGAAGAG TTGCTGGCCT 180

AGCGGTGTTT CATGGGAAAC TCTTAGATGG ATTCTTCATT CGACCATTCT ACAAGATGAT 240

GCTGGGGAAG CAGATAACGC TGAACGACAT GGAGTCCGTG GACAGCGAGT ACTACAACTC 300

TTTGAAGTGG ATCTTAGAAA ACGACCCCAC GGAACTTGAC CTCATGTTCT GCATAGACGA 360

GAGAACTTTG GGCAGACATA CCAAGTGGAT CTGAAGCCCA ACGGGTCAGA AATAATGGTA 420

ACCAATGAGA ACAAACGAGA ATACATTGAC TTAGTCATCC AGTGGAGATT TGTGAACAGG 480

GTCCAGAAGC AAATGAATGC CTTCTTGGAG GGATTTACAG AACTTCTTCC AATCGACTTG 540

ATTAAAATTT TTGATGAAAA TGAGCTGGAG TTGCTGATGT GCGGCCTTGG TGATGTCGAC 600

GTGAACGACT GGAGACAGCA CTCTATTTAC AAGAACGGCT ACTGCCCCAA CCACCCTGTC 660

ATCCAGTGGT TCTGGAAGGC CGTGCTCCTG ATGGATGCTG AGAAGCGCAT CCGGTTACTA 720

CAGTTTGTCA CAGGCACCTC CAGAGTACCC ATGAATGGAT TTGCCGAACT CTATGGTTCC 780

AATGGTCCTC AGCTGTTTAC AATAGAGCAA TGGGGCAGTC CGAAAAACTA CCAGAGCTCT 840

ACATGCTTAA TCGC

854

- (2) INFORMATION FOR SEQ ID NO: 4:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 604 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

- His Ala Cys Ser Asn Ala Ala Ser Arg Ala Ala Ala Arg Val Ala Ala 1 5 10 15
- Arg Cys Thr Ala Arg Ser Arg Ser Gly Arg Arg Ser Ser Ser Val Ser 20 25 30
- Arg Ser Ser Ser Arg Gly Ala Ser Ser Ser Met Ser Ser Asp Met Ala 35 40 45
- Ala Asp Ser Ala Val Ser Asp Val Trp Cys Asp Lys Thr Asp Gly Gly 50 55 60
- Gly Ser Gly Ser Asp Val Thr Asp Thr Cys Cys Gly Cys Trp Asn Asn 65 70 75 80
- Ser His Val Thr Ala Asp Tyr His Asn Asp Asp Thr Arg Val Val Arg 85 90 95
- Val Lys Val Ala Gly Gly Ala Lys Lys Asp Gly Ala Ser Asp Tyr Val 100 105 110
- Arg Val Thr Tyr Asp Met Ser Gly Thr Ser Val Thr Lys Thr Lys Lys 115 120 125
- Ser Asn Lys Trp Asn Arg Val Arg His Arg Val Asp Asn Arg Thr Arg 130 135 140
- Asp Asp Gly Val Asp Val Tyr Thr Asn Arg Met Arg Tyr Thr Lys Asp 145 150 155 160
- Val His Arg Ser His Lys Ser Arg Val Lys Gly Tyr Arg Lys Met Thr
 165 170 175
- Tyr Lys Asn Gly Ser Asp Asn Ala Asp Ala Gly Trp Val Val Asp Asp 180 185 190
- Ala Ala Thr His His Ser Gly Trp Arg Asp Val Gly Arg Thr Tyr Tyr 195 200 205
- Val Asn His Ser Arg Arg Thr Trp Lys Arg Ser Asp Asp Asp Thr Asp 210 215 220
- Asp Asn Asp Asp Met Ala Arg Ala Thr Thr Arg Arg Ser Asp Val Asp 225 230 235 240
- Gly Asp Asn Arg Ser Asn Trp Val Arg Asp Asn Thr Tyr Ser Gly Ala 245 250 255

- Val Ser Ser Gly His Asp Val Thr His Ala Asn Thr Arg Ala Val Cys 260 265 270
- Gly Asn Ala Thr Ser Val Thr Ser Ser Asn His Ser Ser Arg Gly Gly 275 280 285
- Ser Thr Cys Thr Val Thr Ser Ser Gly Gly Trp Lys Asp Asp Arg Gly 290 295 300
- Arg Ser Tyr Tyr Val Asp His Asn Ser Lys Thr Thr Trp Ser Lys 305 310 315 320
- Thr Met Asp Asp Arg Ser Lys Ala His Arg Gly Lys Thr Asp Ser Asn 325 330 335
- Asp Gly Gly Trp Arg Thr His Thr Asp Gly Arg Val Asn His Asn Lys 340 345 350
- Lys Thr Trp Asp Arg Asn Val Ala Thr Gly Ala Val Tyr Ser Arg Asp 355 360 365
- Tyr Lys Arg Lys Tyr Arg Arg Lys Lys Lys Thr Asp Asn Lys Met Lys 370 375 380
- Arg Arg Ala Asn Asp Ser Tyr Arg Arg Met Gly Val Lys Arg Ala Asp 385 390 395 400
- Lys Ala Arg Trp Asp Gly Lys Gly Asp Tyr Gly Gly Val Ala Arg Trp
 405 410 415
- Ser Lys Met Asn Tyr Tyr Gly Tyr Ser Ala Thr Asp Asn Tyr Thr Asn 420 425 430
- Asn Ser Gly Cys Asn Asp His Ser Tyr Lys Gly Arg Val Ala Gly Met 435 440 445
- Ala Val Tyr His Gly Lys Asp Gly Arg Tyr Lys Met Met Lys Thr His 450 455 460
- Asp Met Ser Val Asp Ser Tyr Tyr Ser Ser Arg Trp Asn Asp Thr Asp 465 470 475 480
- Arg Asp Gly Thr His His Lys Thr Gly Gly Ser Val Val Thr Asn Lys 485 490 495
- Asn Lys Lys Tyr Tyr Val Trp Arg Val Asn Arg Lys Met Ala Ala Lys 500 505 510

Gly Asp Lys Asp Asn Met Cys Gly Gly Asp Val Asp Val Asn Asp Trp 515 520 525

Arg His Thr Lys Tyr Lys Asn Gly Tyr Ser Met Asn His Val His Trp 530 535 540

Trp Lys Ala Val Trp Met Met Asp Ser Lys Arg Arg Val Thr Gly Thr 545 550 555 560

Xaa Ser Arg Val Met Asn Gly Ala Tyr Gly Ser Asn Gly Ser Thr Val 565 570 575

Trp Gly Thr Asp Lys Arg Ala His Thr Cys Asn Arg Asp Tyr Ser Asp 580 585 590

Trp Asp Lys Met Ala Asn Thr Gly Asp Gly Val Asp 595 600

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 615 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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CCCCAAAGTG CCTGGCCACC CCTCCCTCCC TGGATCACTG CTGCCTGGGC TTGATTGATT 120

GATTGATTGA TTGATTGATT GATTTTGAGA GAGATTCTCA CTGTCACCCA GGCTGGAGTA 180

CAGTGGTGCG ATCTCGGCTC ACTGCAGCCT CTGCCTCCCG GGTTCAAGCA ATTCTCCTGC 240

CTCAGCCTCC CAAGTAGCTG GGACTACAGG CACGCGCCAC CACACCCAGC TAATTTTGTA 300



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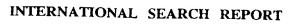
GGATGCTCCA GGCCT

615

INTERNATIONAL SEARCH REPORT

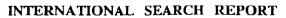
Internat. Application No PCT/GB 98/02259

A. CLASSI IPC 6	FICATION OF SUBJECT MATTER C12N15/00 C07K14/435 C12N9/	10 C12Q1/68		
According to	o International Patent Classification (IPC) or to both national class	sification and IPC		
	SEARCHED			
IPC 6	comentation searched (classification system followed by classific CO7K C12N			
Documenta	tion searched other than minimum documentation to the extent th	at such documents are included in the fields s	searched	
Electronic d	sata base consulted during the international search (name of data	base and, where practical, search terms use	a;	
C. DOCUM	ENTS CONSIDERED TO BE RELEVANT			
Category '	Citation of document, with indication, where appropriate, of the	relevant passages	Relevant to claim No	
X,P	WO 97 37223 A (UNIV NORTH CAROL 9 October 1997	WO 97 37223 A (UNIV NORTH CAROLINA) 9 October 1997		
А	see abstract see page 9, line 1 - page 10, 1 see figure 23 see claim 48 see Nos.125 and 126 of Sequence	18-21		
X,P	OHARA O. ET AL.: "Prediction of sequences of unidentified human VIII. The complete senquences of cDNA clones from brain which callarge proteins in vitro" EMBL DATABASE.5 December 1997. HEIDELBERG. DE AC: ABOO7899	1,2,4. 8-10,18, 21		
	~	,		
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X Furt	ther documents are listed in the continuation of box C	X Patent tamily members are liste	d in annex	
* Special categories of cried documents." "A" document defining the general state of the lart which is not considered to be of particular relevance." "E" earlier document but published on or after the international filling date. "L" document which may throw doubts on priority iclaim(s) or which is cited to establish the publication date of another citation or other special reason (as specified). "O" document referring to an oral disclosure, use, exhibition or other means. "P" document published prior to the international filling date but later than the priority date claimed.		or priority date and not in conflict will cited to understand the principle or i invention "X" document of particular relevance; the cannot be considered novel or can involve an inventive step when the c "Y" document of particular relevance; the cannot be considered to involve an document is combined with one or i ments, such combination being obv- in the air.	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is Taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled	
	actual completion of the international search	Date of mailing of the international s	search report	
<u></u>	11 December 1998	12/01/1999		
Name and	making address of the ISA European Patent Office, P.B. 5818 Patentiaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Authorized officer Panzica, G		



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C.(Continu	ation) DOCUMENTS CONSIDERED TO BE RELEVANT	PCT/GB 9	8/02259
Calegory '	Citation of document, with indication, where appropriate, of the relevant passages		
	appropriate, of the relevant passages		Relevant to claim No
A	STINE O.C. ET AL.: "Evidence for linkage of bipolar disorder to chromosome 18 with a parent-of-origin effect" AMERICAN JOURNAL OF HUMAN GENETICS, vol. 57, no. 6, 1995, pages 1384-1394, XP002087610 US cited in the application see the whole document		
A	MORS O. ET AL.: "Cytogenetic abnormalities on chromosome 18 associated with bipolar affective disorder or schizophrenia" BRITISH JOURNAL OF PSYCHIATRY, vol. 170, March 1997, pages 278-280, XP002087611 GB		
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Information on patent family members

Internat i Application No PCT/GB 98/02259

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Patent docum		Publication date		atent family member(s)	Publication date	
WO 973722	23 A	09-10-1997	AU	2659797 A	22-10-1997	